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Pred. No.

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AUTHORS TITLE JOURNAL

Dunbar, J., Takala, S., Barns, S.M., Davis, J.A. and Kuske, C.R. Levels of bacterial community diversity in four arid soils compared by cultivation and 16s rRNA gene cloning Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Dunbar, J., Takala, S., Barns, S.M., Davis, J.A. and Kuske, C.R.
Direct Submission
Submitted (15-FBB-1999) Environmental Molecular Biology, Life
Sciences Division, Los Alamos National Laboratory, M888, Los
Alamos, NM 87545, USA
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Soil clone WD5 16S ribosomal
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Alamos, NM 87545, USA
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Dunbar, J., Takala, S., Barns, S.M.,
Direct Submission
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Dunbar, J., Takala, S., Barns, S.M., Davis, J.A. and Kuske, C.R.

Levels of bacterial community diversity in four arid soils compared
by cultivation and 16S xRNA gene cloning

Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
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Direct Submission
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Submitted (08-SEP-2000) Faculty of Agricultural and
Riological Sciences, Gent University, Coupure Links
2 (bases 1 to 440)
Dunbar, J., Takala, S.,
Direct Submission
Submitted (15-FEB-199)
                                                                                                         Dunbar, J., Takala, S., Barns, S.M., Davis, J.A. Levels of bacterial community diversity in f by cultivation and 16s rRNA gene cloning Appl. Environ. Microbiol. 65 (4), 1662-1669
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1 (bases 1 to 440)
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On Sep 8, 2000 this sequence version replaced gi:9864056
Location/Qualifiers
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Dejonghe, W.L., Goris, J., El
Verstraete, W. and Top, E.M.
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Submitted (23-MAR-2000) Faculty of Agricultural and
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Dejonghe, W.L., Goris, J., E
Verstraete, W. and Top, E.M.
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Sphingomonadaceae; environmental samples.
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|mol_type="genomic DNA"
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AF280951
Uncultured bacterium
sequence.
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Phylogenetic relationships among yeasts of the 'Saccharomyces complex' determined from multigene sequence analyses
FEMS Yeast Res. 3 (4), 417-432 (2003)
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495 bp DNA linear PLN 11-JUN-2003
Tetrapisispora arboricola small subunit ribosomal RNA gene, partial
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Kurtzman, C.P. and Robnett, C.J.
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/mol_type="genomic DNA"
/db_xref="taxon:92278"
/clone="C0108"
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/strain="NRRL Y-27308"
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New perspective on uncultured bacterial phylogenetic
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3 (bases 1 to 500)
Stach, J.E., Bathe, S. and Burns, R.G.
Direct Submission
Submitted (20-JUN-2000) Biosciences, University Submitted (20-JUN-2000) Rosciences, University Rd, Canterbury, Kent CT2
Location/Qualifiers
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1 (bases 1 to 500)
Stach, J.E., Bathe, S., Clapp, J.P. and Burns, R.G.
PCR-SSCP comparison of 16S rDNA sequence diversity in soil DNA obtained using different isolation and purification methods FEMS Microbiol. Ecol. 36 (2-3), 139-151 (2001)
                                                                                                                                                                       Submitted (10-DEC-2002) Molecular, Cellular and Developmental Biology, University of Colorado, Campus box 347, Boulder, CO 80309,
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                                                                                                                                                                                                         Harris, J.Kirk., Kon Direct Submission
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/mol_type="genomic DNA"
/db_xref="taxon:77133"
/product="16S ribosomal RNA"
                                                         /mol type="genomic DNA"
/isolation_source="marine
/db_xref="taxon:77133"
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Harris,J.Kirk, Kelley,S.T. and J. Harris,J.Kirk, Kelley,S.T. and J. Harris,J.Kirk, Kelley,S.T. and Jevelopmental Direct Submission
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                                                                                                                                                       Unpublished
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Harris, J.Kirk., Kelley, S.T. and Pace, N.I
New perspective on uncultured bacterial
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/mol type="genomic DNA"
/isoTation_source="contaminated aquifer"
/db xref="taxon:174293"
/clone="WSA86"
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RNA gene, partial sequence.
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Pred. No. 3.5e+02;
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AY293558
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AF442312 534 bp DNA linear PLN 11-JUN-2003 Tetrapisispora iriomotensis small subunit ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product. AF442312
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Uncultured phototrophic eukaryote clone FL14G11 16S ribosomal RNA
gene, partial sequence; chloroplast gene for chloroplast product.
AY293558
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-MAY-2003) Geology, University of Illinois,
Natural History Building, 1301 West Green St, Urbana, IL
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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1 (bases 1 to 529)
Bonheyo, G.T., Fouke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Frias-Lopez,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonheyo, G.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chloroplast uncultured phototrophic eukaryote uncultured phototrophic eukaryote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frias-Lopez,J.
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larity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                            /organism="uncultured phototrophic
/organelle="plastid:chloroplast"
/mol_type="genomic DNA"
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/mol_type="genomic_DNA"
/isoTation_source="contaminated aquifer"
/db_xref="taxon:77133"
                                                                                                                                                                                                                                                                  /product="16S ribosomal
                                                                                                                                                                                                                                                                                                             db_xref="taxon:172788"
clone="FL14G11"
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                                                                                                                                                                                                     Score 21; DB 3;
Pred. No. 3.5e+02;
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                                                                                                                                                                                                                      Length 529;
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JOURNAL
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1 (bases 1 to 550)

1 (bases 1 to 550)

Dunbar, J., Takala, S., Barns, S.M., Davis, J.A. and Kusk Dunbar, J., Takala, S., Barns, S.M., Davis, J.A. and Kusk Levels of bacterial community diversity in four arid by cultivation and 16S rRNA gene cloning by cultivation and 16S rRNA gene cloning Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
AF128705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kurtzman,C.P. and Robnett,C.J.

Phylogenetic relationships among yeasts of the 'Saccharomyces complex' determined from multigene sequence analyses

FEMS Yeast Res. 3 (4), 417-432 (2003)
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Tetragisispora iriomotensis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccha
Eukaryota; Fungi; Ascomycotaceae; Tetrapisispora.
                                                                                                                                                                                                             2 (bases 1 to 550)
Dunbar, J., Takala, S., Barns, S.M., Davis, J.A.
Direct Submission
                                                                                                                                                           Sciences Division, Los Alamos National Alamos, NM 87545, USA
                                                                                                                                                                                               Submitted (15-FEB-1999) Environmental
                                                                                                                                                                                                                                                                                                                                                                                             uncultured soil bacterium S0212 uncultured soil bacterium S0212 Bacteria; environmental samples.
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Similarity 100.0%;
21; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organelle="mitochondrion"
/mol_type="genomic DNA"
/strain="NRRL Y-27309"
                                               /organism="uncultured soil bacterium S0212"
|mol_type="genomic DNA"
|db xref="taxon:92327"
|clone="50212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="small subunit ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:113606"
/clone="A315"
               /product="16S ribosomal
                                                                                                                                        ocation/Qualifiers
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Pred. No.
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                                                                                                                                                                            Molecular Biology,
l Laboratory, M888,
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SOURCE
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Furlong,M.A., Singleton,D.R., Coleman,D.C. and Whitman,W.B. Molecular and culture-based analyses of prokaryotic communifrom an agricultural soil and the burrows and casts of the earthworm Lumbricus rubellus Appl. Environ. Microbiol. 68 (3), 1265-1279 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-NOV-2001) United States Department of Agriculture, National Center for Agricultural Utilization Research, 1815 N. University St., Peoria, IL 61604, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetrapisispora nanseiensis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Tetrapisispora.
                                                                                                                        uncultured soil bacterium uncultured soil bacterium
                                                                                                                                                                                                                            AY037640 559 bp Uncultured soil bacterium clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phylogenetic relationships among yeasts of the 'Saccharomyces complex' determined from multigene sequence analyses FEMS Yeast Res. 3 (4), 417-432 (2003)
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Tetrapisispora nanseiensis small subunit ribosomal RNA gene
                                                                                     Bacteria; environmental samples.

1 (bases 1 to 559)
                                                                                                                                                                              AY037640.1 GI:15789072
                                                                                                                                                                                               partial sequence.
AY037640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="NRRL Y-27310"
/db_xref="taxon:113607"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="small subunit ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Tetrapisispora nanseiensis"
organelle="mitochondrion"
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Pred. No. 3.4e+02;
; Mismatches 0;
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S133 16S ribosomal RNA gene,
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                                      communities of the
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AY193243
LOCUS
DEFINITION
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VERSION
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Search completed: August 4, 2004, 07:44:21 Job time: 921.446 secs
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11872477
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Harris, J. Kirk., Kelley, S.T. and Pace, N.R.
Direct Submission
Submitted (10-DEC-2002) Molecular, Cellular and Developmental
Biology, University of Colorado, Campus box 347, Boulder, CO 80309,
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Oncultured bacterium clone Bol43 16S ribosomal RNA gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Conservative
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1 (bases 1 to 564)
Harris, J. Kirk., Kelley, S.T. and Pace, N.R.
New perspective on uncultured bacterial phylogenetic division OP11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uncultured bacterium uncultured bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (31-MAY-2001) Department of Microbiology, University of Georgia, 541 Biological Sciences Bldg, Athens, GA 30602-2605, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 559)
Singleton, D.R., Furlong, M.A., Coleman, D.C. and Whitman, W.B.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                                    100.0%; Score 21; DB 1; ilarity 100.0%; Pred. No. 3.4e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                              /product="168 ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:164851"
                                                                                                                                                                                                                                                                                               /organism="uncultured bacterium"
imol type="genomic DMA,"
isolation, source="marine sediment"
idb_xref="taxon:77133"
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Sequence 7, Appli
Sequence 3170, Ap
Sequence 3171, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 755, Appli
Sequence 758, Appli
Sequence 5, Appli
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Sequence 476, Appli
Sequence 476, Appli
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                                                            Sequence 7, Application US/08227475

Patent No. 5521674

GENERAL INFORMATION:
APPLICANT: Hoshina, Sadayori
APPLICANT: Hoshina, I Bernard
TITLE OF INVENTION: Microorganism
TITLE OF INVENTION: Microorganism
TITLE OF INVENTION: Oligomers
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                         RESULT 2
US-08-227-475-7,
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US-09-073-465-9
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Best Local S
Matches 20
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Patent No. 6054278
GENERAL INFORMATION:
APPLICANT: DODGE, Deborah E
APPLICANT: SNITH, Doug
TITLE OF INVENTION: RIBOSOMAL RNA GENE POLYMORPHISM BASED MICROORGANISM
TITLE OF INVENTION: IDENTIFICATION
FILE REFERENCE: 4343 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/073,465
CURRENT FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Unknown Organism FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Unknown Organism: Bacterial
 COMPUTER READABLE FORM:
                                    STREET: 30 Rocke
CITY: New York
STATE: New York
              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                            Local Similarity
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ilarity 100.0%;
Conservative C
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US-09-175-932A-5
US-09-171-099-5
US-09-13-377B-2
US-09-13-377B-2
US-09-191-099-6
US-09-191-099-6
US-09-191-099-6
US-09-191-099-2
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US-09-191-099-2
US-09-191-099-2
US-09-193-377B-4
US-09-193-377B-4
US-09-193-377B-7
US-08-252-470-27
US-09-193-377B-8
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Pred. No. 0.016;
Mismatches (
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying

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US-09-577-640-3
US-09-577-640-3
US-09-328-111-75
US-09-328-111-728
US-09-328-111-450
US-09-06-089-3
US-09-06-089-3
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US-09-101-94-13
US-08-632-470-50
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US-09-191-099-4
US-09-191-099-4

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Query Match

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SUMMARIES

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US-09-073-465-9 US-08-227-475-7 US-09-107-532A-3170

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Scoring table: Sequence:

OLIGO\_NUC Gapop 60.0 ,

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277475446 residues Gapext 60.0 Perfect score:

US-09-940-860-1 20

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RESULT 3
US-09-107-532A-3170/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3170, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: (212) 422523 COOP
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local
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APPLICATION NUMBER: US 07/672
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 3454
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: N
                                                                   APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
COMPUTER: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                  OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID A ENTEROCOCCUS F
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 GCAAACAGGATTAGATACCC 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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                                                                                                                                                                                                                                                                          COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212) 664-0525
212) 422523 COOP UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (212) 977-9550
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                                                                                                                                                                                                                                                                                                                                              USA
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Pred. No. 0.014;
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 195;
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NAME/KEY: misc feature; LOCATION: (B) LOCATION 1...279; SEQUENCE DESCRIPTION: SEQ ID NO: 3170: US-09-107-532A-3170
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (781)893-5007
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3170:
SEQUENCE CHARACTERISTICS:
                                                                                                            TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3171:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinifello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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ADDRESSEE: GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCAAACAGGATTAGATACCC 20
                                                        LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 Beaver Street
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100.0%; Prr
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Pred. No. 0.014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORPORATION
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NAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...279;
SEQUENCE DESCRIPTION: SEQ ID NO: 3171;
US-09-107-532A-3171
                                             US-09-577-640-3
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US-08-979-586-3
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                                                                 RESULT 6
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GENERAL INFORMATION:
APPLICANT: Weinste
              Sequence 3, Application Patent No. 6420165
                                                                                                                                                                                    Matches
                                                                                                                                                                                                     Query Match
Best Local (
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52208/JPW/JKM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,586
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: oth HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 538 base pairs
TYPE: nucleic acid
STRANDEDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Weinstein, TITLE OF INVENTION: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                 234 GCAAACAGGATTAGATACCC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 GCAAACAGGATTAGATACCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                       1 GCAAACAGGATTAGATACCC 20
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                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                 100.0%; Score 20; DB 3; ilarity 100.0%; Pred. No. 0.013; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                       NO
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                                                                                                                                                                                                                                                                                                        other nucleic acid
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100.0%; Pred. No. 0.014;
ative 0; Mismatches
                              US/09577640
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M CAPABLE OF BIODEGRADATION OF
                                                                                                                                                                                                                   DB 3; Length 538;
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CURRENT APPLICATION NUMBER: US/09/577,640
COURRENT FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 08/979,586
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0 - beta
SEQ ID NO 3
LENGTH: 538
TYPE: DNA
ORGANISM: Bacillus midousuji
US-09-577-640-3
                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 755
LENGTH: 571
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                          ; OTHER INFORMATION: n = A, T, C
US-09-328-111-755
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Best Local Similarity
Matches 20; Conserve
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                                                                        Matches
                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Steinmann, Kathleen E. APPLICANT: Astle, Jon H. APPLICANT: Burgess, Christopher C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 755,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: The Trustees of Columbia University in the City of TITLE OF INVENTION: Bacterium Capable of Biodegradation of Wastes FILE REFERENCE: 52208apct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Derti, Adnan
APPLICANT: Ford, Doma M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS FILE REFERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Carroll III, Eddie APPLICANT: Catino, Theodore J.
                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(571)
                                                          Local 5.
295
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                                                                                       Similarity
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                       GCAAACAGGATTAGATACCC 20
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GCAAACAGGATTAGATACCC 314
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                                                                  100.0%; Silarity 100.0%; FConservative 0;
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G
                                                                      Score 20; DB
Pred. No. 0.0
0; Mismatches
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RESULT 8 US-08-953-171-2 ; Sequence 2, Application US/08953171 ; Patent No. 6124094

ENERAL INFORMATION:

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APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
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                                                                                                                                                                                                                                                                                               APPLICANT: APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: STAPLETON, RAYMOND
APPLICANT: STAPLETON, RAYMOND
APPLICANT: STAPLETON, RAYMOND
APPLICANT: SAYLER, GARY
APPLICANT:
APPLI
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FILING DATE: 17-OCT-1997
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ZOOGLOEAL AND HYPH
TITLE OF INVENTION: SPP. NUCLEIC ACIDS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 404 688 0770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Spratt, Gwendolyn DD REGISTRATION NUMBER: 36,016 REFERENCE/DOCKET NUMBER: 05
JCANT: Lewis, Marcia E.
JCANT: Monahan, John E.
JCANT: Schlegel, Robert
JE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
JE OF INVENTION: PRODUCTS
REFERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 404 688 9880
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5. 6262333
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Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
                                                                                                                                                                                                                                                                                                                                                                                                   Steinmann, Kathleen E. Astle, Jon H.
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                                                                                                                                                                                                   Derti, Adnan
Ford, Donna M.
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127 Peachtree Street, N.E., Suite 1200
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LAYTON, ALICE
KELLY, CHIRSTINE
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Pred. No. 0.013;
; Mismatches
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                                                                                             US-08-114-695A-5
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CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 728
Query Match
Best Local Similarity 85.0
""" hes 17; Conservative
                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08114695A Patent No. 5508193
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Best Local S
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NAME/KEY: misc_feature
LOCATION: (1)...(624)
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                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/114,695A FILING DATE: 31-AUG-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,5
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Wackett, Lawrence P.
TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
TITLE OF INVENTION: WATER
NUMBER OF SEQUENCES: 8
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                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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ZIP: 55402
                                                                                                                  ORGANISM:
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STREET: 3500 IDS CENTER
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                       100.0%; Score 20; DB 1; Length 660; 85.0%; Pred. No. 0.013; tive 3; Mismatches 0; Indels
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Pred. No. 0.013;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07898905
Patent No. 5424187
GENERAL INFORMATION:
APPLICANT: Shor;Kuo
TITLE OF INVENTION: "DIAGNOSIS AND TREATMENT OF ARTERIAL
TITLE OF INVENTION: CHLAMYDIAL GRANULOWA"
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christeensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
TELEFAX: 1-206-224-0779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIF: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTHARE: PastSEQ for Windows Version 3.0
SEQ ID NO 450
LENGTH: 672
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CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/07/698,
FILING DATE: 19920612
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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ATTORNEY/AGENT INFORMATION:
NAME: SUNDERMO, JOHN, S.
REGISTRATION NUMBER: 34,446
REFRENCE/DOCKET. NUMBER: UFW
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
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TYPE: nucleic acid
                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-328-111-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
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TELEX: 4
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US-07-898-905-1
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                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Burges, Christopher C.
APPLICANT: Burges, Christopher C.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll Manan
APPLICANT: Carroll Macria E.
APPLICANT: Cord, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION NUMBER: US 60/088,801
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER APPLICATION NUMBER: 1998-06-10
NUMBER OF SEQ ID NOS: 850
CORD IN NO. 4.75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

100.0%; Score 20; DB 3; Length 665;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 20; Conservative 0; Mismatches 0; Indels
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Sequence 450. Application US/09328111

GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Burges, Christopher C.
APPLICANT: Carroll III, Eddie
APPLICANT: Bord, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN
TITLE OF INVENTION: NOVEL HUMAN
TITLE OF INVENTION: NOVEL HUMAN
TITLE OF INVENTION: NOWER: US/09/328,111
CURRENT APPLICATION NUMBER: US/09881
                                                                                                                                                                               Sequence 476, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
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LCCATION: (1)...(665)

CTHER INFORMATION: n = A,T,C or G

US-09-328-111-476
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                                      50 GCAAACAGGAUUAGAUACCC 69
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ORGANISM: Homo sapiens
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US-09-328-111-476
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US-09-328-111-450
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LENGTH: 665
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             US-07-899-905-2
; Sequence 2, Application US/07898905
; Patent No. 5424187
; Patent No. 5424187
; GARBEAL INFORMATION:
; APPLICANT: Shor; Kuo
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seattle
; STATE: Hashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 851
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Sequence 3, Application US/07898905
Batent NO. 5424187
GENERAL INTERMATION:
APPLICANT: Shor;Kuo
TITLE OF INVENTION: "DIAGNOSIS AND TREATMENT OF ARTERIAL
TITLE OF INVENTION: CHLAMYDIAL GRANULOMA"
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/898,905
FILING DATE: 19920612
CLASSIFICATION DATA:
APPLICATION NUMBER: none
FILING DATE: none
FILING DATE: none
ATTORNEY ARPLICATION: 34,446
APPLICATION NUMBER: 34,446
REGISTRATION NUMBER: 34,446
REGISTRATION NUMBER: 1056-6224-0727
TELEX: 1-206-622-8100; 1-206-224-0727
TELEX: 4-30103-23
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 851 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
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Best Local Similarity 100.0
Matches 20; Conservative
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ZIP: 98101-2347
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MOLECULE TYPE: 9

DESCRIPTION: 0
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US-07-898-905-3
RESULT 14
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COMPUTER: IEM PC/386 Compatible
OPERATING SYSTEM: Mac-OS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/899,905
FILING DATE: 10-350612
PRILASSIFTCATION: 435
PRILASSIFTCATION NUMBER: none
FILING DATE: none
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Sequence 35, Appl
                                                                                                    4, 2004, 06:01:54; Search time 39.759 Seconds (without alignments) 307.073 Million cell updates/sec
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1. /cgn2 6/ptodata/2/ina/5A_COMB.seq:*

2. /cgn2 6/ptodata/2/ina/6B_COMB.seq:*

3. /cgn2 6/ptodata/2/ina/6A_COMB.seq:*

4. /cgn2 6/ptodata/2/ina/6B_COMB.seq:*

5. /cgn2 6/ptodata/2/ina/6B_COMB.seq:*

5. /cgn2 6/ptodata/2/ina/egucknB_Seq:*

5. /cgn2 6/ptodata/2/ina/egucknB_Seq:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-07-923-871C-35
US-07-923-871C-1
PCT-US91-01574-1
US-09-052-333A-26
US-09-052-333A-27
US-09-052-333A-29
US-09-052-333A-29
US-09-052-333A-29
US-09-052-333A-29
US-09-052-333A-29
US-08-632-470-40
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US-08-632-470-32
US-08-632-470-34
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3-08-632-470-28
3-08-632-470-29
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                                                                        nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 2, Ag
Sequence 1, Ag
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Sequence 49, P
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 Sequence 43, Sequence 46, Sequence 38, Sequence 30, Sequence 53, Sequence 53, Sequence 44,
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Sequence 1, A
Sequence 1, A
Sequence 2, A
Sequence 1, A
Sequence 1, A
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Sequence 36, Application US/07923871C
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: White Ph.D, Thomas J.
APPLICANT: Dodge, Deborah E.
TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 368
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,871C
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2 US-08-632-470-43
2 US-08-632-470-46
2 US-08-632-470-36
2 US-08-632-470-36
2 US-08-632-470-45
2 US-08-632-470-44
4 US-09-198-452A-1
1 US-08-943-464-1
1 US-08-943-464-1
1 US-08-943-464-2
4 US-09-491-384-1
4 US-09-491-384-1
2 US-09-61-770-1
2 US-08-633-470-48
2 US-08-633-470-48
                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTONEY/AGENT INFORMATION:
NAME: PETY, DOUGHGR A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8697
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-07-923-871C-36
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   1440 2 1441 2 1441 2 1442 2 1442 2 1468 2 1 1508 2 1 683 1 1
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complement (41)
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LOCATION: compler
FEATURE:
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LOCATION:
FEATURE:
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NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
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LOCATION:
US-07-923-871C-1
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                                                                                                                                   RESULT 2
US-07-923-871C-35/C

Sequence 35, Application US/07923871C

Sequence 35, Application US/07923871C

Patent No. 5912117

GENERAL INFORMATION:
APPLICANT: Bodge, Deborah E.
TITLE OF INVENTION:
APPLICANT: Dodge, Deborah E.
TITLE OF INVENTION:
APPLICANT: Dodge, Deborah E.
TITLE OF INVENTION:
STREEP: 340 Kingsland for Diagnosis of Lyme Disease
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREEP: 340 Kingsland Street
CITY: Nutley
STATE: USA
COUNTRY: USA
COUNTRY
COUNTRY: USA
COUNTRY
COU
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APPLICANT: White Ph.D, Thomas J.
APPLICANT: White Ph.D, Thomas J.
APPLICANT: Dedge, Deborah E.
TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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340 Kingsland Street
273 ACAAGGCCCGAGAACGTATTCA 252
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; Sequence 1, Application US/07923871C
; Patent No. 5912117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 22; Conservative
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Matches
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100.0%; Score 22; DB 3; Length 1284;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Domain I of the 23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Region A - Region of the Intergenic Spacer"
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; OTHER INFORMATION: /note= "Region B - The 3' End of ; OTHER INFORMATION: Domain I in the 23S rRNA"
US-09-052-333A-26
                                                                                                              COMPUTER FEADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: FLODS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
CLASSIFICATION CURTES P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0211.97
TELEPAN: 309/681-6513
TELEPAN: 309/681-658
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LEMOTH: 1284 base pairs
TYPE: ILLOLeic asingle
STRANDEDNESS: single
TYPE: Lincation Linear
MATEGRATION COMPANIANE
SEQUENCE CHARACTERISTICS:
LEMOTH: 1284 base pairs
TYPE: ILLOLeic asingle
TYPE: ILLOLeic asingle
TYPE: ILLOLeic asingle
TYPE: ILLOLeic asingle
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TOPOLOGY: Linear
MOLECULE TYPE: FRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
GRGANISM: CNlamydia pneumoniae
STRAIN: CWL-029
FEATURE:
NAME/KEY: FRNA
LOCATION: 1..221
OTHER INFORMATION: /note= "168 fRNA"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 222..444
OTHER INFORMATION: /note= "intergenic spacer"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: TRNA
LOCATION: 445..1284
OTHER INFORMATION: /note= "23S fRNA"
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OTHER INFORMATION: /
FEATURE:
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                                                                   COUNTRY: US
ZIP: 61604
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TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS: ADDRESSEE: Curtis P. Ribando
STREET: 1815 N. University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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OPERATING STGIEM: PC-DOS/MS-DOS
OFFRANT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01574
FILING DATE: 19910307
CLASSIFICATION: 435
PRICAR APPLICATION: 435
PRICAR APPLICATION: 435
PRICAR APPLICATION: 435
PRICAR APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1590
ATTONNEY/AGENT INFORMATION:
NAME: KASTCE*, KEVIN R:
REGISTRATION NUMBER: 2536.1
FELERHONE: (415) 420-3444
TELEPHONE: (415) 658-5239
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO AMTI-SERSE: NO
FRATILERED.
FRATILERED
                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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LOCATION:
FEATURE:
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LOCATION:
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FEATURE:
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; Sequence 27, Application US/09052333A; Patent No. 6261769

Gaps

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NAME/KEY: misc_RNA
LOCATION: 1.1537
OTHER INFORMATION: /note= "Region A - Region of the
OTHER INFORMATION: Intergenic Spacer"
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LOCATION: 222..444
OTHER INFORMATION: /note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..221
OTHER INFORMATION: /note= "16S rRNA"
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OTHER INFORMATION: /note= "23S rRNA"
                                                                                                                                                                               US-09-052-333A-28/c

Sequence 28, Application US/09052333A

Patent No. 6261769

GENERAL INFORMATION:
                                                                          67 ACAAGGCCCGAGAACGTATTCA 46
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ORIGINAL SOURCE:
ORGANISM: Chlamydia pneumoniae
STRAIN: FWL-12
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                                                                                                                                                         RESULT 7
GENERAL INFORMATION:
APPLICANT: Everett, Karin D.E.
APPLICANT: Andersen, Arthur A.
TITLE OF INVENTION: Intergenic Spacer Target Sequence for TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains NUMER OF SEQUENCE: 73
NUMBER OF SEQUENCE: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 N. University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 22; DB 3; Length 1284; Best Local Similarity 100.0%; Pred. No. 3.9e-05; Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: rRNA
LOCATION: 445..1063
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_RNA
LOCATION: 1..537
COTHER INFORMATION: /note= "Region A - Region of the OTHER INFORMATION: Intergenic Spacer"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: rRNA

1.0CATION: 959..1086

OTHER INFORMATION: /note= "Region B - The 3' End of

OTHER INFORMATION: Domain I in the 23S rRNA"

US-09-052-333A-27
                                                                                                                                                                                                                                                                                       STATE: FEO.IG
STATE: LL
COUNTRY: US
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
CLASSIFICATION NUMBER: US/09/052,333A
ATTORNEY/AGENT INFORMATION:
NAME: RIDBANGO, CURTIS P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0211.97
TELEPHONE: 309/681-6688
INFORMATION PROR SEQ ID NO: 27:
SEGUENCE CHRARACTERISTICS:
LENGTH: 1284 base pairs
TTYPE: NUCLEIC acid
STRANDBRESS: Single
STRANDBRESS: Single
STRANDBRESS: Single
STRANDBRESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: rRNA
LOCATION: 445..1284
OTHER INFORMATION: /note= "23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: JENA
NAME/KEY: 1..221
COCATION: 1..221
OTHER INFORMATION: /note= "16S fRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Chlamydia pneumoniae
STRAIN: CWL-1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_RNA
LOCATION: 222.7444
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: rRN
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                              STREET: 1815
CITY: Peoria
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GENERAL INVENTATION:
APPLICANT: Beverett, Karin D.E.
APPLICANT: Andersen, Arthur A.
APPLICANT: Andersen, Arthur A.
THILE OF INVENTION: Intergenic Spacer Target Sequence for FITTE OF INVENTION: Intergenic Spacer Target Sequence for STRAET: 112 OF INVENTION: Detecting and Distinguishing Chlamydial Strains NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSE: Curtis P. Ribando
STREET: 1815 N. University Street
STREET: 1816 N. University Street
NOBECULE TYPE: 1081 N. NO.
ANTI-SENSE N. NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAMEKEY: rRNA
LOCATION: 445..1063
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
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OTHER INFORMATION: /note= "Domain I of the 23S rRNA" FEATURE:
                                                                                                                     NAME/KEY: TRNA
LOCATION: 445..1284
OTHER INFORMATION: /note= "23S rRNA"
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1815 N. University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 acaacccccadaaccrarrca 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-052-333A-31/c
; Sequence 31, Application US/09052333A
Patent No. 6261769
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Chlamydia pneumoniae
STRAIN: TW-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: rRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
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| Sequence 29, Application US/09052333A
| Patent No. 6261769
| GENERAL INFORMATION:
| APPLICANT: Everett, Karin D.E. |
| APPLICANT: Andersen, Arthur A. |
| TITLE OF INVENTION: Intergenic Spacer Target Sequence for TITLE OF INVENTION: Intergenic Spacer Target Sequence for TITLE OF EQUENCES: 73
| VUMBER OF SEQUENCES: 73
| CORRESPONDENCE ADDRESS: |
| ADDRESSE: Curtis P. Ribando |
| STREET: 1815 N. University Street |
| CITY: Peoria |
| STATE: IL |
| STA
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                 ; FEATURE:
; NAME/KEY: rENA
; LOCATION: 959..1086
; OTHER INFORMATION: /note= "Region B - The 3' End of
; OTHER INFORMATION: Domain I in the 23S rRNA"
US-09-052-333A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 61604

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: rRNA
LOCATION: 1..221
OTHER INFORMATION: /note= "16S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECTLE TYPE: rRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia pneumoniae
STRAIN: FML-16
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 ACAAGGCCGAGAACGTATTCA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: R.Dando, Curtis P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0211.
TELECOMMUNICATION INFORMATION:
TELEFAX: 309/691-6513
TELEFAX: 309/691-6618
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1284 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_RNA
LOCATION: 222..444
OTHER INFORMATION: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: rRNA
LOCATION: 445..1063
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US-09-052-333A-29/c
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APPLICANT: Breett, Karin D.E.
APPLICANT: Andersen, Arthur A.
TITLE OF INVENTION: Intergenic Spacer Target Sequence for
PATENTE OF INVENTION: Detecting and Distinguishing Chlamydial Strains
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSE: Curtis P. Ribando
                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 22; DB 3; Length 1284; Best Local Similarity 100.0%; Pred. No. 3.9e-05; Matches 22; Conservative 0; Mismatches 0; Indels 0
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 1.537
CTHER INFORMATION: /note= "Region A - Region of the OTHER INFORMATION: Intergenic Spacer"
FEATURE:
NAME/KEY: RNA
                                                                                                                                                                                      LOCATION: 959.1086
OTHER INFORMATION: /note= "Region B - The 3' End of CTHER INFORMATION: Domain I in the 23S rRNA"
US-09-052-333A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: 11
STATE: 11
COUNTRY: US
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OFFWARE: PETENTIN PC-DOS/MS-DOS
SOFFWARE: PETENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
CLASSIFICATION: 435
ATTONREY/AGNET INPORMATION:
NAME: Ribando, Curtis P.
REGISTRATION NUMBER: 27,976
REGISTRATION NUMBER: 27,976
REGISTRATION NUMBER: 0211.97
TELEPHONE: 309/681-6513
TELEPHONE: 309/681-6688
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1284 base pairs
TYPE: MOLOLE acid
STRANDEDNESS: single
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Gaps

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GENERAL INFORMATION:
APPLICANT: AMBLIAT, CLAUDE
APPLICANT: AMBLIAT, CLAUDE
APPLICANT: RADILAT, DIDIER
TITLE OF INVENTION: NUCLECTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: UA
ZIP: 22320
                                                                                                                                                                                                                                                                             Length 1408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-UUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                        100.0%; Score 22; DB 2; I
100.0%; Pred. No. 3.9e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 22; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET UNHER: WPB 38238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-277
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1427 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1319 ACAAGGCCCGAGAACGTATTCA 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACAAGGCCCGAGAACGTATTCA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application US/08632470 Patent No. 5976791 GENERAL INFORMATION:
APPLICANT: MABILAT, CLAUDE
                                            STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-632-470-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-08-632-470-27/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-632-470-25/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND THEIR USE AS PROBES OR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 22; DB 3; Length 12
100.0%; Pred. No. 3.9e-05;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-632-470-40/c
; Sequence 40, Application US/08632470
; Patent NO. 5976791
; GENERAL INFORMATION:
APPLICANT: MABILAT, CLAUDE
APPLICANT: RAOULT, DIDIER
; TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETT
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETT
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 445..1063
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
| NAME/KEY: misc RNA | LOCATION: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STALE.

COUNTRY: USA
ZIP: 22320
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08 JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGNT INFORMATION:
NAME: BERRIDGE, WILLIAM P
REFERENCE/DOCKET WIMBER: WPB 38238
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFOR
                                                                                                                                                                                                                       LOCATION: 222.7444
OTHER INFORMATION: /note= "intergenic spacer"
                                       LOCATION: 1..221
OTHER INFORMATION: /note= "16S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: rRNA
LOCATION: 445..1284
OTHER INFORMATION: /note= "235 rRNA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                     misc_RNA
                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: rRNA
                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EATURE:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: MABILAT, CLAUDE

APPLICANT: MADULT, DIDIER

TITLE OF INVENTION: HYBREDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND

TITLE OF INVENTION: HYBREDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND

TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIFF & BERRIDGE

STREET: P.O. BOX 19928

CITY: ALEXANDRIA

STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 08-JUL-1996

CLASSIFICATION: 435

ATTONENT/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P

REGISTRATION NUMBER: 30,024

RELECOMMUNICATION INFORMATION:

TELEPHONE: (703)-936-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 22; DB 2; I Best Local Similarity 100.0%; Pred. No. 3.9e-05; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 22; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0;
                     ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P
REGISTARTION NUMBER: 30,028
REFERENCE/DOCKET NUMBER: WPB 38238
TELECOMMUNICATION INFORMATION:
TELEFONE: (703)-836-6400
TELEFONE: (703)-836-277
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1327 ACAAGGCCCGAGAACGTATTCA 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-632-470-34/c
; Sequence 34, Application US/08632470
; Patent No. 5976791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACAAGGCCCGAGAACGTATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-632-470-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703)-836-2781
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 1436 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) US-08-632-470-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 1436 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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Fatent No. 5976791

GENERAL INFORMATION

APPLICANT: MABILAT, CLAUDE

APPLICANT: RACULT, DIDIER

TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS

TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS

TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS

CORRESPONDENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSE: OLIFF & BERRIDGE

STREET: P.O. BOX 19928

COUNTRY: USA

STATE: VA

STATE: VA

MEDIUM TYPE: Floppy disk

COMPUTER REDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Datentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/632,470

FILING DATE: 08-JUL.1996

CLASSIFICATION: 435
                                                         NUCLEOTIDE FRAGMENTS CAPABLE OF
HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
THEIR USE AS PROBES OR PRIMERS
53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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APPLICANT: RACULT, DIDIER
TITLE OF INVENTION: NUCLECTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
NUMBER OF SQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSED OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STRATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER: IDEP PC COMPACIBLE
MEDIUM TYPE: Floppy disk
COUNTRY: WAS
COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) US-08-632-470-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-632-470-32/c
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1331 ACAAGGCCCGAGAACGTATTCA 1310

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GENERAL INFORMATION:
APPLICANT: MABILAT, CLAUDE
APPLICANT: ARADIT, DIDIER
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                  STREET: P.O. BOX 19928

STATE: VA.
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-UUL-1996
CLASSIPICATION: 435
ATTORNEY AGENT INPORMATION:
NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
RELEPHONE: (703)-836-6400
TELEPHONE: (703)-836-6787
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: MUCICIC acid
STRANDEDNESS: single
RESULT 15
VS-08-632-470-24/c
Sequence 24, Application US/08632470
Patent No. 5976791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-632-470-24
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; 0 Gaps ; 0 Query Match
100.0%; Score 22; DB 2; Length 1438;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0; Indels ( ò

1 ACAAGGCCCGAGAACGTATTCA 22

1333 ACAAGGCCCGAGAACGTATTCA 1312

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Search completed: August 4, 2004, 09:23:29 Job time : 40.759 secs

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28
                                                                                                                                                 August 4, 2004, 06:01:54; Search time 36.1446 Seconds (without alignments) 307.073 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                             682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Listing first 45 summaries
                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                       US-09-940-860-2
20
1 ggaggaaggcgaggatgacg 20
                                                                                                                                                                                                                                                                                                                             OLIGO NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	H 4	٠٢.	П	110	Sequence 13336, A	13193,	12614,	11226,	11111,	50	82	'n	ď	ς,	Sequence 2, Appli	7	'n	62	equence 6369,	6182	e 2, Ar	٦,	670	equence 13, App	223	32,
ΩI	US-	79-052- 09-052-	-09-198-4	19-252-991A-11	-09-252-991A-1333	-09-252-991A-1319	-09-252-991A-126	US-09-252-991A-11226	-09-252-991A-11	-9917	-09-621-976-857	1	-08-818-111	-09-056-556	US-09-072-596-2	-09-072-967	US-09-050-739~5	US-09-252-991A-6286	-09-252-	US-09-252-991A-6182	US-09-103-840A-2	US-09-103-840A-1	-09-252-991A-	-09-743-207-	-09-252-991A-2	US-09-252-991A-10382
DB		<b>1</b> M	44	4	4	4	4	4	4	4	4	m	4	4	4	4	4	4	4	4		m	4	4	4	4
% Query Match Length		2762	1230025	420	1107	1179	1308	1683	1974	2283	191	752	752	752	752	752	889	1245	1980	4	037	4411529	g)	4	738	885
% Query Match	100	100.0	റ	0	80.0	0	80.0	80.0	0	80.0	S	75.0	75.0	75.0	75.0	75.0	'n	75.0	75.0	'n.	75.0	75.0	ö	°.	70.0	70.0
Score	000	0 0	20	16	16	16	16	16	16	16	15	15	15	15	15	15	15	15	15	15	15	15	14	14	14	14
Result No.	, 	7 M	4	ľ	φ υ	0 7	<b>0</b> 0		c 10	11	c 12	13	14	15	16	17	18	Н	c 50	21	22	23	c 24	c 25	26	c 27

c 28 14 70.0 1206 4 US-09-489-033A-4798 c 29 14 70.0 1206 4 US-09-52-991A-6674 23 14 70.0 1774 4 US-09-573-355A-11 c 31 14 70.0 2016 4 US-09-52-91A-2465 33 14 70.0 2164 4 US-09-52-91A-6671 c 35 14 70.0 2164 4 US-09-52-91A-6671 c 35 14 70.0 2169 4 US-09-52-91A-6671 c 36 14 70.0 2169 4 US-09-52-91A-6671 c 37 14 70.0 2677 4 US-09-52-91A-6671 c 38 14 70.0 2677 4 US-09-26-69-67-312-1 c 49 14 70.0 2677 4 US-09-26-26-26-1 c 41 14 70.0 17138 4 US-09-26-64-31-1 c 42 14 70.0 3477 4 US-09-26-64-31-1 c 41 14 70.0 17138 4 US-09-26-64-31-1 c 42 14 70.0 43950 4 US-09-26-64-31 c 42 14 70.0 43950 4 US-09-26-64-31 c 43 14 70.0 43950 4 US-09-26-64-31 c 45 15 65.0 20 4 US-09-26-64-31 c 45 17 65.0 20 4 US-09-26-64-31 c 5	Sequence 4798, Ap Sequence 6674, Ap Sequence 2607, App Sequence 2445, Ap Sequence 2445, Ap Sequence 10268, A Sequence 1, Appli Sequence 3, Appli	pug .	Length 1548;  Indels 0; Gaps 0;  quence for g Chlamydial Strains
	28 14 70.0 1206 4 US-0 30 14 70.0 1260 4 US-0 31 14 70.0 1717 4 US-0 33 14 70.0 2016 4 US-0 34 14 70.0 2016 4 US-0 35 14 70.0 2163 4 US-0 36 14 70.0 2163 4 US-0 37 14 70.0 2163 4 US-0 38 14 70.0 2637 4 US-0 39 14 70.0 2637 4 US-0 40 14 70.0 3437 3 US-0 41 70.0 3437 3 US-0 41 70.0 17138 3 US-0 42 14 70.0 17138 4 US-0 43 14 70.0 17138 4 US-0 44 14 70.0 17138 4 US-0 45 14 70.0 17138 4 US-0 46 14 70.0 43950 4 US-0 47 14 70.0 43950 4 US-0	SumenTS cterial Method 5,774 150 n 4.0	Ob-726-7/4-11  Duery Match Best Local Similarity 100.0%; Score 20; DB 4; Le Best Local Similarity 100.0%; Pred. No. 0.015; Matches 20; Conservative 0; Mismatches 0;  1 GAGGAAGGCGAGGATGACG 20

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linea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 3; Length 2751; 100.0%; Pred. No. 0.015; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37, Application US/09052333A

Patent No. 6561769

GENERL INFORMATION:
APPLICANT: Everett, Karin D.E.
APPLICANT: Andersen, Arthur A.
PITLE OF INVENTION: Intergenic Spacer Target Sequence for Patent No. 6561769

TITLE OF INVENTION: Detecting and Distinguishing Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: rRNA
LOCATION: 789..1409
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 346.7881
OTHER INFORMATION: /note= "Region A - Region of the OTHER INFORMATION: Intergenic Spacer"
FRATURE:
FRATURE:
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1303...1432
OTHER INFORMATION: /note= "Region B - The 3' End of corner information: Domain I in the 23S rRNA"
US-09-052-333A-6
                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1..564
OTHER INFORMATION: /note= "16S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: FRNA
LOCATION: 789.2751
OTHER INFORMATION: /note= "23S FRNA"
                                                                                                                    FILING LAYER
CLASSIFICATION:
ATTORNEY/ACENT INFORMATION:
NAME: RIDAND, CLARIS P.
REGISTRATION NUMBER: 27,976
REGISTRATION NUMBER: 0211.97
TELECHONEUNICATION INFORMATION:
TELECHONEUNICATION INFORMATION:
TELECHONE 309/681-688
INFORMATION FOR SEG ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2751 base pairs
TYPE: nucleic acid
STRANBENBES: single
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: rRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia psittaci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 GGAGGAAGCCGAGGATGACG 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc RNA
LOCATION: 565.788
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-09-052-333A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Op
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Detecting and Distinguishing Chlamydial Strains

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 20; DB 3; Length 2762;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 803..1424
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: 1320..1447
; OTHER INFORMATION: /note= "Region B - The 3' End of correct Information: Domain I in the 23S rRNA" US-09-052-333A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /note= "Region A - Region of the OTHER INFORMATION: Intergenic Spacer"
                                                                                                                                                                   COMPUTER READBALE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTING SYSTEM: PC-DOS/MS-DOS
SOFTIMER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/0S2,333A
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_RNA.
LOCATION: 565..802
OTHER INFORMATION: /note= "intergenic spacer"
FRATURE:
NAME/KEY: rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: rRNA
LOCATION: 1..564
OTHER INFORMATION: /note= "16S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: rRNA
LOCATION: 803..2762
OTHER INFORMATION: /note= "23S rRNA"
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 N. University Street
CITY: Peoria
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: FRNA
HYPOTHETICAL: NO
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia trachomatis
STRAIN: R22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 GCAGGAAGGCGAGGATGACG 212
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INN: 133
ATTORNEY/AGENT INN: 135
NAME: Ribando, Curtis P.
REGISTRATION NUMBER: 27,976
REPERENCE/DOCKET NUMBER: 0211
TELECOMMUNICATION INFORMATION:
TELEFRAN: 309/681-688
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 2762 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGAGGAAGGCGAGGATGACG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_RNA
LOCATION: 346..895
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
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LOCATION: (270001)...(285000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (285001)...(30000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (300001)...(31500)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (315001)...(33000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (330001)...(34500)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (330001)...(36000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (345001)...(36000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (360001)...(37500)

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NAME/KEY: misc feature
LOCATION: (330001)...(37500)

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NAME/KEY: misc feature
LOCATION: (330001)...(37500)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (330001)...(375000)

OTHER INFORMATION: n=a or c or g or t
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CATION: (456001)..(465000)

CATION: (456001)..(480000)

CATION: (456001)..(480000)

HERE INFORMATION: n=a or c or g or t WE/KEY: misc feature

CATION: (480001)..(495000)

CATION: (480001)..(495000)

MEN INFORMATION: n=a or c or g or t WE/KEY: misc feature

CATION: (480001)..(495000)
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LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (630001)..(645000)
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LOCATION: (585001)..(60000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
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IION: (435001)..(450000)
R INFORMATION: n=a or c or g or
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LOCATION: (52501)...($4000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: ($40001)..($5500)
LOCATION: ($40001)..($5500)
LOCATION: ($55001)..($7000)
LOCATION: ($5501)..($7000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: ($7000)
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LOCATION: (600001)..(615000)
DTHER INFORMATION: n=a or c or g
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IION: (420001)..(435000)
R INFORMATION: n=a or c or g
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LOCATION: (495001)..(510000)
OTHER INFORMATION: n=a or c or g
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NION: (405001)..(420000)
RINFORMATION: n=a or c or g
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ION: (390001)..(405000)
INFORMATION: n=a or c or g
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NAME/KEY: misc_feature
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LOCATION: (51001)..(525000)
OTHER INFORMATION: n=a or c or
                                                                                                                                            APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT APPLICATION NUMBER: US/09/198,452A
SURBER OF SEQ ID NOS: 6849
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (225001)..(240000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (90001)..(105000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (195001)..(210000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (60001). (75000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (13501)..(150000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (45001)..(60000)
JTHER INFORMATION: n=a or c or g or
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LOCATION: (120001)..(135000)
OTHER INFORMATION: n=a or c or g or
                                                          Sequence 1, Application US/09198452A Patent No. 6559294 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KRY: misc_feature
LOCATION: (1)...(15000)
OTHER INFORMATION: n=a or c or g
LOCATION: (15001)...(30000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (150001)..(165000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (165001)..(180000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (180001)..(195000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (25501)..(270000)
OTHER INFORMATION: n=a or c or g
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (240001) .. (255000)
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           RESULT 4
US-09-198-452A-1
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NS-09-152-991A-13356/c

| Sequence 13356, Application US/09252991A
| Sequence 13356, Application US/09252991A
| Sequence 13356, Application US/09252991A
| PAPLICANT: Marc J. Rubenfield et al. |
| APPLICANT: Marc J. Rubenfield et al. |
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| PRIOR FILING DATE: 1999-02-18 |
| PRIOR PLICATION NUMBER: US 60/094,190 |
| PRIOR PLICATION NUMBER: US 60/094,190 |
| PRIOR FILING DATE: 1999-07-27 |
| NUMBER OF SEQ ID NOS: 33142 |
| SEQ ID NO 13336 |
| LENGTH: 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-09-252-991A-13193/C
US-09-252-991A-13193/C
Squence 13193, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
APPLICATION WINDER: US/09/252,991A
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPREBENCE: 107196,136
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-0-18
PRIOR FILING DATE: 1998-0-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13193
LENGTH: 1179
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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 16; DB 4; Length 1107; 100.0%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 16; DB 4; Length 420; 100.0%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                     FILE REFERENCE: 107196.136
CURRENT APPLICATION WUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11029
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Prea. ...
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                                                                                                                                                                                                                                                                                                                          TYPE: DNA
) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
, ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 GAAGGCGAGGATGACG 123
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Best Local Similarity 100.
Matches 16; Conservative
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US-09-252-991A-11029
US-09-252-991A-1029, Application US/09252991A
; Sequent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (66001)..(67500)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (67501)..(69000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (69001)..(69000)
OTHER INFORMATION: n=a or c or g or t
OTHER INFORMATION: n=a or c or g or t
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (180001)...(795000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (79501)...(81000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (81001)...(82500)
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NAME/KEY: misc feature
LOCATION: (81001)...(82500)
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NAME/KEY: misc feature
LOCATION: (84000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (85501)...(85500)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (85501)...(87000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (85501)...(88500)
                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (705001). (720000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (720001). (735000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (735001)..(75000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (750001)..(765000)
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LOCATION: (765001)..(780000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (900001)...(915000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or g or t
   OTHER INFORMATION: n=a or c or g or
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Sequence 11111/c
sequence 11111, Application US/09252991A
sequence 11111, Application US/09252991A
sequence 11111, Application US/09252991A
sequence 11111, Application US/09252991A
setent No. 6551795
sequence 11111, Application Sequences Relating To Pseudomonas TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
release TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
release TITLE OF INVENTION NUMBER: US/09/252,991A
current Application NUMBER: US/09/252,991A
prior Filing Date: 1998-02-18
prior Filing Date: 1998-02-18
prior Filing Date: 1998-07-27
prior Filing Date: 1998-07-27
seq ID NO: 33142
seq ID NO: 11111
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APPLICANT:
MATC J. RUDEHFIELD & C. A.I.
APPLICANT:
MATC J. RUDEHFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGATIOS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PAPLICATION NUMBER: US 60/074,788
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10956
LENGTH: 2283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
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100.0%; Pred. No. 2.4;
.ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Sequence 10956, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1856 AGGAGGCGAGGATGA 1871
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Matches 16; Conserv
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US-09-252-991A-10956
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US-09-621-976-8573/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-11111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. RUCERIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11226
LENGTH: 1683
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196-136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 12614

LENGTH: 1308
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                                                                                                   Length 1179;
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2.4;
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Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.09-252-991A-11226/c
Sequence 11226, Application US/09252991A
Patent No. 6551795
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100.0%; Pro
; TYPE: DNA; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13193
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ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                 196 GAAGGCGAGGATGACG 181
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Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
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APPLICANT: Dillon, Davin C...
APPLICANT: Campos-Neto, Antonia
APPLICANT: Gampos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Towniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
VUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS: 48
CORRESPONDENCE ADDRESS: 48
CORRESPONDENCE ADDRESS: 148
COUNTRY: Gattle
STATE: Weakington
COUNTRY: USA
ZIP: 98104-77092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTE: FALANABLE FORM:
MEDILIM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Parent BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REFERENCE/DOCKET NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 31.392
TELEPHONE: (206) 622-4900
                                                                                                                                                                   US-08-818-111-2
; Sequence 2, Application US/08818111
; Patent No. 6338852
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Best Local Similarity 100.0%; Pr
Matches 15; Conservative 0;
                                                                                                                                                                                                                                                          APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                          434 AAGGCGAGGATGACG 448
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 752 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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75.0%; Score 15; DB 3; Length 752;
Best Local Similarity 100.0%; Pred. No. 98.5;
Matches 15; Conservative 0; Mismatches 0; Indels
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DatentIn Release #1.0, Version #1.30
CURBENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIPICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REFERRENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
FILE REFERENCE: GENSET.054PR2
CURRENT PEPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8573
LENGTH: 191
                                                                                                                                                                                                                                 NAME/KEY: misc_feature

LOCATION: 2

COTHER INFORMATION: n=a, g, c or t

US-09-621-976-88573
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 752 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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US-08-818-112-2
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                                                                                    ABOULD A STREET: 6300 Columbia Center, 701 Fifth Avenue
75.0%; Score 15; DB 4; Length 752; 100.0%; Pred. No. 8.5; 0; Indels tive 0; Mismatches 0; Indels
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CITY: Seattle
STATE: Washington
COUNTRY: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-Dos/MS-Dos
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-ARR-1998
CLASSIFICATION:
ATTORNATION NUMBER: US/09/056,556
FILING DATE: 07-ARR-1998
FREIERRANCH/DOCKET NUMBER: 210121.457
FELECOMMUNICATION INFORMATION:
TELEPHORE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-2
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Search completed: August 4, 2004, 09:23:28 Job time: 42.1446 secs

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Sequence 4, Appli
Sequence 78545, A
Sequence 27667, A
Sequence 1484, Ap
Sequence 3179, Ap
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Sequence 35039, A
Sequence 1280, Ap
Sequence 352, App
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31366, A
1477, Ap
1478, Ap
1478, Ap
                                                                                                                              August 4, 2004, 07:44:29; Search time 190.012 Seconds (without alignments) 541.892 Million cell updates/sec
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/ Ggn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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/ Ggn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-437-965-78545
US-10-437-965-78545
US-10-489-1484
US-09-535-459-1484
US-09-919-197-10
US-10-425-114-3639
US-09-854-867-352
US-10-425-114-1420
US-10-425-114-1420
US-09-535-459-1477
US-09-535-459-1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                         3222919 segs, 2451570024 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                                       nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                              Sequence:
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                                                                                                                                     Run on:
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No.
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Sequence 1	41773 Sequence 4	137746 Sequence 1	137747 Sequence 1	137748 Sequence 1	137746 Sequence 1	137747 Sequence 1	137748 Seguence 1	1481 Sequence 1	124900 Sequence 1	3413 Seguence 3	315667. Sequence 2	215668 Sequence 2	215667 Sequence 2	215668 Sequence 2	S27 Sequence	70931 Sequence 7	164886 Sequence 1	164887 Seguence 1	164888 Sequence 1	164886 Sequence 1	164887 Sequence 1	164888 Sequence 1	-2049 Sequence 2	12225 Sequence 1	16650 Seguence 1	311 Sequence 2	-33705 Sequence	34553 Sequence	17503 Sequence 1	•
09-535-459	7 US-10-437-96	3 US-10-027-632	3 US-10-027-632	3 US-10-027-632	6 US-10-027-632	6 US-10-027-63	6 US-10-027-632	0 US-09-535-459	3 US-10-424-59	7 US-10-021-32	3 US-10-027-63	3 US-10-027-63	6 US-10-027-632	6 US-10-027-632	7 US-10-333-184	7 US-10-437-963	3 US-10-027-632	3 US-10-027-632	3 US-10-027-63	6 US-10-027-6	6 US-10-027-63	6 US-10-027-63	2 US-10-152-31	3 US-10-425-11	3 US-10-425-11	3 US-10-389-64	3 US-10-282-122	6 US-10-369-49	3 US-10-42	16 US-10-408-167A
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Sequence 4, Application US/08940860; Sequence 4, Application WO. US200400055581
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL GAPPLICAMT: Rothman, Malindar, Maulik
TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
FILE REPERENCE: 01107.00185;
GURRENT APPLICATION NUMBER: US/09/940,860
CURRENT APPLICATION NUMBER: 00/229,376
FRIOR APPLICATION NUMBER: 60/229,376
FRIOR APPLICATION NUMBER: 60/229,376
FRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: synthetic amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
RESULT 1
US-09-940-860-4
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1 GTGCCAGCAGCAGCGGTAATA 21 à 유

21; Conservative

Matches

Query Match Best Local Similarity

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Gaps

;; 0

Indels

100.0%; Score 21; DB 11; Length 21; 100.0%; Pred. No. 0.02;

0; Mismatches

RESULT 2
US-10-437-963-78545/c
Sequence 78545, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

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APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Rebecca B.
APPLICANT: Naughton, Rebecca B.
FILE COF INVENTION: POLYNUCLECTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE FILE COF INVENTION: DOLYNUCLECTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE CURRENT APPLICATION NUMBER: US/09/535,459
CURRENT APPLICATION NUMBER: 100-03-24
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2170
SOFTWARE: PERL Program
SOFTWARE: PERL Program
ELENGTH: 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosanne M. Crooke
APPLICANT: Mark J. Graham
TITLE OF INVENTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
FILE REFERENCE: ISPH-0593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Feng, Paul C.C.
APPLICANT: Feng, Paul C.C.
APPLICANT: Encher, Karen L.
APPLICANT: Sincher, Karen L.
APPLICANT: Jegels, Todd B.
TITLE OF INVENTION: Nacleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
RIOR APPLICATION NUMBER: US 60/255, 619
RIOR PILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NOS: 17880
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                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01212406
US-09-535-459-1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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, OTHER INFORMATION: Clone ID: LIB3825-023-Q6-K6-G3
US-10-021-323-3179
                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.2%; Score 16; DB 10;
100.0%; Pred. No. 13;
iive 0; Mismatches 0;
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CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3179, Application US/10021323 Publication No. US20040123340A1 GENERAL INFORMATION: APPLICANT: Deikman, Jili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09919197
Publication No. US20030083484A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 TGCCAGCAGCAGCGGT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 GCCAGCAGCAGCGGTA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -10-021-323-3179/c
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US-09-919-197-10
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                                                                                                                                                                                                             and Other Molecules Associated With
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Willer Sarry S.
APPLICANT: Goldman, WILL Barry S.
APPLICANT: Goldman, WILL Barry S.
APPLICANT: Goldman, WILL Barry S.
APPLICANT: Goldman, WILL BARRSION OF MICROBIAL PROFERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROFERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PRILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 27667
LENGTH: 3502
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Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 17; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 16; Length 3502;
Pred. No. 3.5;
0; Mismatches 0; Indels
                                                                                                                                                APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other J
TITLE OF INVENTION: Plants and Uses Thereof for Plant Imp
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4530_78341C.1
US-10-437-963-78545
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US-09-535-459-1484
US-09-535-459-1484
Sequence 1484, Application US/09535459
Publication No. US20030040615A1
GENERAL INFORMATION:
La Rosa, Thomas J.

Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
Wu, Wei
Boubharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1018 CAGCAGCAGCGGTAATA 1002
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Best Local Similarity 100.0%; P. Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 CAGCAGCAGCGGTAATA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-369-493-27667
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -10-369-493-27667/c
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APPLICANT:
APPLICANT:
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Sequence 352, Application US/09854867

Sedication No. US2030224356A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOAN, KNOLL H

APPLICANT: ROGAN, PETER K

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
TITLE OF INVENTION: 0003-05-08
CURRENT APPLICATION UNDER: US/09/854,867

CURRENT APPLICATION UNDER: US/09/854,867

CURRENT FILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 613

SOFTWARE: PATENTIN Version 3.1

SEQ ID NO 352

LENGTH: 1992
                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Pred. No. 13;
                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_101161C.1
VG-10-437-863-1280
                                                                                           FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1837)
OTHER INFORMATION: unsure at all n locations
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LOCATION: (1)..(1992)
OTHER INFORMATION: 11pa15_5
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LOCATION: (1418)..(1418)
OTHER INFORMATION: n is a,
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; LOCATION: (1802)
; OTHER INFORMATION: n is a,
US-09-854-867-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (760)..(760)
OTHER INFORMATION: n is a,
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LOCATION: (1149)..(1149)
OTHER INFORMATION: n is a,
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LOCATION: (1558)..(1558)
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (1533)..(1533)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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OTHER INFORMATION: n is
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PEATURE:
NAME/KEY: misc feature
'...Ton: (760)...(760)
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ORGANISM: Oryza sativa
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ORGANISM: Homo sapiens
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les 16; Conserv
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Matches
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwel
APPLICANT: W. Wei
APPLICANT: Buukharov, Andrey A.
APPLICANT: Buukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zhou, Tihua Zhou, Toka Zhou, Toka Zhou, Yongwai Zhou, Yon
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red. No. 13;
Mismatches 0; Indels
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13;
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; OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE032D03_FLI
US-10-425-114-35039
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 1119
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Best Local Similarity 100.0%; Fred. No.
Matches 16; Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                   Query Match 76.2%; Score 16; Best Local Similarity 100.0%; Pred. No. Matches 16; Conservative 0; Mismatc
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Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays subsp. mexicana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 GTGCCAGCAGCAGCGG 176
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                                                                                                  TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                        FEATURE:

NAME/KEY: CDS

LOCATION: (33)...(815)

US-09-919-197-10
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Sequence 1477, Application US/09535459

Publication No. US20030040615A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebeca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REQULATING ELECTRON TRANSFER MOLECULE FILE REFERENCE: PO-1014 CIP APPLICANTION NUMBER: US/09/535,459
CURRENT PILING DATE: 2000-03-24
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PATCHIN Version 3.1
SEQ ID NO 31366
LENGTH: 3672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.4%; Score 15; DB 10; Length 280; 100.0%; Pred. No. 48; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu00988392
US-09-535-459-1477
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Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTGCCAGCAGCAGCGG 16
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                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Pseudomonas putida
US-10-282-122A-31366
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Matches 16; Conserva
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Matches 15; Conserva
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US-09-535-459-1477/c
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APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Goo, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Dants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 1420
LENGTH: 2329
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Gaps
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0; Indels
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
0; Mismatches
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US-10-425-114-1420
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                                                                                                                                                                         US-10-425-114-1420/c
) Sequence 1420, Application US/10425114
) Publication No. US20040034888A1
) GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
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PRIOR APPLICATION NUMBER: 60/242,578
                                                                           1317 GTGCCAGCAGCAGCGG 1302
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                             1 GTGCCAGCAGCAGCGG 16
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 100.
Matches 16; Conservative
16; Conservative
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ORGANISM: Zea mays
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Matches
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TITLE OF INVENTION: POLYNUCLECTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECUL: FILE REFERENCE: PD-1014 CIP US/09/535,459
CURRENT APPLICATION NUMBER: US/09/535,459
CURRENT APPLICATION NUMBER: 0200-03-24
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2170
SOFTWARE: PERL Program
SEQ ID NO 1479
LENGTH: 391
                                                                                                                                                                                                                                                                                                                                                                                                   71.4%; Score 15; DB 10; Length 391; 100.0%; Pred. No. 48; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01224429
US-09-535-459-1479
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-53-475, Application US/09535459

Sequence 1475, Application US/09535459

Publication No. US20030040615A1

GENERAL INFORMATION:

APPLICANT: Seilhamer, Jeffrey J.

APPLICANT: Stuart, Suran G.

APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYMUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE

FILE REFERENCE: PD-1014 CIP

CURRENT FILING DATE: 2000-03-24

Prior application data removed - consult PALM or file wrapper

SOFTWARE: PERL Program

SEQ ID NO 1475

LENGTH: 364

LENGTH: 364
     APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
FILE REPREBNCE: PD-1014 CIP
CURRENT APPLICATION NUMBER: US/09/535,459
CURRENT APPLICATION NUMBER: US/09/535,459
PRIOR APPLICATION ADDIA - CON0-03-24
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2170
SOFTWARE: PERL Program
SEQ ID NO 1478
LENGTH: 296
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US-09-535-459-1478
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US-09-535-459-1475
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US-09-535-459-1479/c
Sequence 1479, Application US/09535459
Publication No. US20030040615A1
GENERAL INFORMATION:
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APPLICANT: Delegeane, Angelo M.
APPLICANT: Strart, Susan G.
Stuart, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Murine DL
Clone VGT
DNA (SeqI
Drosophil
Rice leaf
cDNA (Seq
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Abz38180 N. gonorr
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3373863 seqs, 2124099041 residues
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Gapop_60.0 , Gapext 60.0
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11: geneseq11980s:*
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Maximum DB seq length: 200000000
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                                                                                                                              OM nucleic
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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'n	Aav02903 Human DNa	Aaa98876 Human pro	Aaa98158 Human pro	^	Abl17969 Drosophil	Abq77568 Human ATP	Aax22772 Human SOC	Aax22778 Human SOC	Aav29137 Homo sapi	Acc44418 Gene enco	Aca47979 Prokaryot	Aaz20095 Cytokine	in	Adb63487 Human cDN	Aaz98625 Silkworm	Aaz20096 Cytokine	Abl07099 Drosophil	Abl28180 Drosophil	Abt06279 Human NOV	Abt06280 Human NOV	Add78281 Human CGD
																		,			
ACA45835	AAV02903	AAA98876	AAA98158	AAD29987	ABL17969	ABQ77568	AAX22772	AAX22778	AAV29137	ACC44418	ACA47979	AAZ20095	AAH17305	ADB63487	AAZ98625	AAZ20096	ABL07099	ABL28180	ABT06279	ABT06280	ADD78281
7	N	m	m	9	4,	9	0	7	(7)	7	7	7	4	σ	ო	~	4	4	9	9	0
1173	1575	1636	1636	1636	1654	1679	1748	1748	1915	2039	2178	2186	2196	2354	2525	2558	2646	2672	lo	2860	2924
71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4
15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15
7	N	~		N					c 33	34	35	c 36	3.7	38	33	۵ 40	c 41	42	c 43	0 44	c 45

## ALIGNMENTS

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This is the nucleotide sequence of one strand of the PSI-PL470 gene of the 30.7 kb extrachromosomal plastid of Plasmodium berghei. This plastid encodes organelle-like rRNAs, trbosomal proteins and RNA polymerase subunits, amongst others. Plasmodium is detected in a human or animal sample by treating it, or derived nucleic acid, with a plasmodium extrachromosomal genetic element or derived nucleic acid (A) and detecting any hybridisation. (A) can include the PSI-PL470, PLH-PPH, PRB
                                                                                                                                               Malaria, infection, therapy, diagnosis, vaccine, plastid, PS1-PL470 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting Plasmodium infection from hybridisation with extrachromosomal element - providing genus or species specific diagnosis with few false negatives, in humans or animals.
                                                                                                                                                                                                                                                                                                                                                                                                                     Tan TMC;
                                                                                                                                                                                                                                                                                                                                                                                                                   Nelson JS,
                                                                                                                   Plasmodium berghei plastid PS1-PL470 gene.
                                                                                                                                                                                                                                                                                                                                                                       (UYSI-) UNIV SINGAPORE NAT.
(MOLE-) INST MOLECULAR & CELL BIOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 54-59; 120pp; English.
               AAV33135 standard; DNA; 5849 BP.
                                                                                                                                                                                           Plasmodium berghei; ANKA strain
                                                                                                                                                                                                                                                                                                                                                                                                                   Tham JM,
                                                                                                                                                                                                                                                                                                            97AU-00004953.
97AU-00006329.
97AU-00009481.
                                                                                                                                                                                                                                                                                 98WO-IB000212.
                                                                                                                                                                                                                                                                                                                                                                                                                   Ting RCY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-447251/38.
                                                                                                                                                                                                                                                                                                            06-FEB-1997;
21-APR-1997;
26-SEP-1997;
                                                                                                                                                                                                                      WO9835057-A1.
                                                                                                                                                                                                                                                                                 05-FEB-1998;
                                                                       17-OCT-2003
07-DEC-1998
                                                                                                                                                                                                                                                     13-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                     Kara AKU,
                                           AAV33135;
AAV33135
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Neisseria meningitidis, Neisseria gonorrhoeae; antigen; vaccine; treatment; Neisseria infection; meningitis; septicaemia; gonorrhea; ss.

Neisseria gonorrhoeae.

W09924578-A2

20-MAY-1999.

Neisseria gonorrhoeae complete ORF139 sequence.

(first entry)

08-OCT-1999

AAZ12223

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RESULT 3 AAZ12223/c ID AAZ12223 standard; DNA; 1542

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and nucleic acids derived from
                                                                                              of genus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records AB237706-AB242016 represent nucleic acid molecules of the invention
              or PWQ gene, the mitochondrial coxI gene, and nucleic acids derived from them. Also new are (A)-specific probes and primers (see AAV33139-56). The method is used to diagnose Plasmodium infection. Also (not claimed) the polygeptides encoded by (A) are useful as targets for drug development and for development of anti-malaria vaccines. The high degree of similarity between (A) from different species allows development of genu-or species-specific assays that result in fewer false negatives than known methods (typically 1% against 3%). (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          manufacture of
                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New protein from Neisseria gonorrheae, useful for the manufact
medicament for treating or preventing N. gonorrheae infection
                                                                                                                                                                               Sequence 5849 BP; 2296 A; 673 C; 557 G; 2323 T; 0 U; 0 Other;
                                                                                                                                                                                                              Score 21; DB 2; Length 5849;
Pred. No. 0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17; DB 7; Length 1458;
Pred. No. 37;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1458 BP; 167 A; 328 C; 569 G; 394 T; 0 U; 0 Other;
                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial; infection; vaccine; gene therapy; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monaci E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. gonorrhoeae nucleotide sequence SEQ ID 949
                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 257; 815pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Masignani V,
                                                                                                                                                                                                                                                                                                               4671 GIGCCAGCAGCAGCGGIAATA 4691
                                                                                                                                                                                                                                                                                 21
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                                                                                                                                                                                                                 100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                     ABZ38180 standard; DNA; 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-2001; 2001GB-00003424
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                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 21, Conservative
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR-) CHIRON SPA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200279243-A2.
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Nucleotide sequences AAZ11972-Z12358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorthoese which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their fragments, their mucleic acids and antibodies are used for diagnosis, prevention (as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster expressed polynucleotide SEQ ID NO 23171.
                                                                                                                                                                                                                                                                                                                                                                                            Proteins from Neisseria meningitidis and N. gonorrhoeae useful diagnosis, treatment and prevention of infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; DB 2; Length 1542; Pred. No. 37; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1542 BP, 175 A, 345 C, 599 G, 423 T, 0 U, 0 Other;
                                                                                                                                                                                                                                                                                                                                  Grandi
                                                                                                                                                                                                                                                                                                                                  Scarlato V,
                                                                                                                                                                                                                                                                                                                                  Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 332; 524pp; English.
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97GB-00024190.
97GB-00024386.
97GB-00025158.
97GB-00025158.
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ12223
                                                                                                                                                                                   09-OCT-1998;
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14-NOV-1997,
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27-NOV-1997
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                    Claim 1; SEQ ID NO 23168; 21pp + Sequence Listing; English.
                          Venter JC, Adams M,
                                                  WPI; 2001-656860/75.
P-PSDB; ABB65459.
 (PEKE ) PE CORP NY
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ADA31033
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                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ss.
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nes 17; Conservative 0
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11-JUL-2000; 2000US-00614150.
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                                       Drosophila melanogaster.
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P-PSDB; ABB65460.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABL01040-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this parent did not form part of the permits of the permits of the form and the control of form part of the form and permits of the form and permits of the form and the control of the contr
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Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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100.0%; Pr
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Best Local Similarity 100.
Matches 17; Conservative
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P-PSDB; ADA35159.
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23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.

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The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as bioconrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                                               76.2%; Score 16; DB 8; Length 684; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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Best Local Similarity
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GENBANK; X62660
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method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic construction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat DNA (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the ovel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal
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Pred. No. 1.1e+02;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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Best Local Similarity 100.
Matches 16; Conservative
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GENBANK; X62660.
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subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polyneptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction in (e.g. spinal segmental nerve injury (Sull) in an animal (e.g. gene therapy). The sequence presented is a rat DNA (shown in Table 2 of the specification) which encodes one of the polypeptides of the invention which is differentially expressed during pain. Note: The sequence data.

Cor this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel compound of 8 - 50 nucleobases in length targeted to a nucleic acid molecule encoding a short heterodimer partner-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antiarteriosclerotic, cardiant, vasotropic, antiinfective, cytostatic, antiinflammatory, inhibitor; antisense gene therapy, atherosclerosis; short heterodimer partner-1; abnormal, lipid, cholesterol metabolism; cardiovascular disease, infection, inflammation, tumour formation; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense oligonucleotide targeted to a nucleic acid encoding short heterodimer partner-1, useful for treating diseases involving abnormal lipid or cholesterol metabolism, e.g atherosclerosis or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Short heterodimer partner-1 expression mouse DNA SEQ ID No 10.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 804 BP; 261 A; 178 C; 198 G; 167 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              76.2%; Score 16; DB 9; Le
100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABT34135 standard; DNA; 1119 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGCCAGCAGCAGCGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-2002; 2002WO-US023245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGCCAGCAGCAGCGG 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-248161/24.
P-PSDB; AAO27109.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    murine; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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I. The novel compound specifically hybridizes with a nucleic acid molecule encoding the short heterodimer partner-1, and inhibits the expression of the nucleic acid molecule. The compound, and a composition comprising it are useful for treating a disease or condition associated with the short heterodimer partner-1, particularly a condition involving abnormal light or cholesterol metabolism such as atherosclerosis or a cardiovascular disease. They are also useful in research and diagnostics for modulating the expression of short heterodimer partner-1. They can also be useful prophylactically in preventing or delaying infection, inflammation or tumour formation. This polynucleotide represents a mouse but sequence relating to the short heterodimer partner-1 of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 28211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                         Sequence 1119 BP; 233 A; 354 C; 289 G; 243 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                Length 1119;
                                                                                                                                                                                                                                                                          Score 16; DB 7; Length 111
Pred. No. 1.1e+02;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                     76.6.
100.001
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                                                                                                                                                                                                                                                                                                                                                                                    161 GTGCCAGCAGCAGCGG 176
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                               1 GIGCCAGCAGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                     Local Similarity 100.
tes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                     Query Match
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The invention relates to an isolated nucleic acid comprising any one of the foll antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiocic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underspressed (12) determining the extent compound's activity; (11) a culture comprising strains in which the strains is present in a culture or collection of the proliferation of an organism; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required
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                                                                                               Gaps
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Xu HH;
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                           Length 2854;
DB 4; Le...
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
Yamamoto R,
                                                                                        Mismatches
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                       76.2%; Score 16;
100.0%; Pred. No.
:ive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prokaryotic essential gene #25153.
                                                                                                                                                                                                                                                                                                                                                                                   ACA43496 standard; DNA; 3672 BP.
                                                                                                                                                                                                     2354 CCAGCAGCGGTAA 2369
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0049231P.
08-FEB-2002; 2002US-00372881.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                         4 CCAGCAGCAGCGGTAA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2002; 2002WO-US009107
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                                                                                        16; Conservative
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Trawick JD,
                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug design; gene.
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Wall D,
                                                                                     Matches
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for cellular proliferation to isolate candidate molecules for rational dup discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. preumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster expressed polynucleotide SEQ ID NO 28208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                            Sequence 3672 BP; 660 A; 1207 C; 1179 G; 626 T; 0 U; 0 Other;
                                                                                                                                                                                                                Length 3672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 28208; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                              76.2%; Score 16; DB 7; Le
100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0;
                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                           1 GTGCCAGCAGCAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                          Query Match 76.2
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
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    88888888888888
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Gaps

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76.2%; Score 16; DB 4; Length 5471; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100. Matches 16; Conservative

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ADD17780;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to deoxyribonuclease (DLAD) proteins and coding sequences, (see AAF60715-6 and AAB72416-7). DLAD is an endonuclease and is capable of divalent cation-independent cleavage of DNA under acidic conditions. DLAD can be used as a substitute for DNase I in treating cystic fibrosis, and is useful in the prevention and treatment of infectious diseases. The present sequence is a PCR primer for murine DLAD signal peptide (AAF60715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viral Jun; v-Jun; cellular Jun; c-Jun; immune system disorder; haematopoietic cell disorder; autoimmune disorder; allergy; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Acidic deoxyribonuclease capable of divalent cation-independent cleavage of DNA under acidic even neutral pH and not inhibited by G-actin, useful in remedies for cystic fibrosis and for treatment of infectious diseases
                                                                                                                                                                                                Murine; DNase; DLAD; deoxyribonuclease; endonuclease; cystic fibrosis; infectious disease; FCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone VGT18 of a gene that is differentially regulated by viral Jun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Preq. ....
                                                                                                                                                                          Murine DLAD signal peptide PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 29; 61pp; Japanese
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                                 3971 CCAGCAGCAGCAGTAA 3986
                                                                                                   BP
                                                                                                                                                                                                                                                                                                              01-MAY-2000; 2000WO-JP002893
                                                                                                                                                                                                                                                                                                                                        99JP-00230870
              4 CCAGCAGCAGCGGTAA 19
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(first entry)
                                                                                         723/c
AAF60723 standard; DNA; 32
                                                                                                                                                  (first entry)
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        Shiokawa
                                                                                                                                                                                                                                                                                                                                                               (TANU/) TANUMA S.
                                                                                                                                                                                                                                                              WO200112793-A1
                                                                                                                                                                                                                                                                                                                                        17-AUG-1999;
                                                                                                                                                                                                                                        Mus musculus.
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06-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                         ranuma S,
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                                                                                                                          AAF60723;
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ID AAF6
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The present sequence is derived from a gene that is differentially regulated by viral Jun (v-Jun) and cellular Jun (c-Jun). The polymucleotide is used to prevent, treat or amelicate a medical condition, e.g. deficiencies or disorders of the immune system, of haemacopoietic cells, autoimmune disorders, allergic conditions, organ rejection or graft-versus-host-disease, inflammation, hyporproliferative disorders, bacterial, fungal, parasitic and virus infections. It can also be used to modulate hemostatic or thrombolytic activity, regenerate tissues, increase chemocaxic activity of cells, modulate mammallan metabolism, change the physical or mental state of a mammal and can be used as food additives to increase or decrease storage capabilities and nutritional components. (Updated on 15-SEP-2003 to standardise OS field)
organ rejection, graft-versus-host-disease, hyperproliferative disorder;
infection, food additive, storage capability; nutritional component; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecules from Gallus domesticus are used for diagnosis and treatment of medial conditions in mammals \varepsilon.g. cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (SeqID 1848) that confers an altered visual phenotype in plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dickerson JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 130 BP; 40 A; 37 C; 30 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bottoli ILC,
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Best Local Similarity 100.0%; Pr
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ADD17780 standard; DNA; 197
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                                                                                                              Gallus gallus.
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(DOWC ) DOW CHEM CO. (DOWC ) DOW AGROSCIENCES LLC.
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Ruegger M, Larrinua I, Shukla V; Crosley R, Skokut T,

WPI; 2003-300858/29.

Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for conferring altered visual phenotypes in plants.

Claim 1; SEQ ID NO 1848; 517pp; English.

This invention relates to the identification and isolation of novel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/ or leaf surface features in plants, such as chlorotic, bleaching, etching, wet leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these novel phenotypes can affect growth regulation i.e. useful for creating dwarf varieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or delayed senescence and also for example produce plants that control the production of ethylene. Purthermore, the present invention comprises generating transgenic plants, as well as reproducibly altering the visual phenotype of plant seeds, plant tissues and plant cells containing the polynucleotides described herein. This polynucleotide is a homologue of a DNA sequence that confers an altered visual phenotype when expressed in plants, the method of the invention. 

Sequence 197' BP; 46 A; 66 C; 42 G; 43 T; 0 U; 0 Other;

Query Match 71.4%; Score 15; DB 9; Length 197; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 15; Conservative 0; Mismatches 0; Indels

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Gaps .; 0

3 GCCAGCAGCAGCGGT 17

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74 GCCAGCAGCAGCGGT 60

Search completed: August 4, 2004, 06:43:39 Job time : 174.554 secs

CK107208 UB49DPG02 AZ677920 ENTHX83TR

AU007074 AU007074

AG65124 GM06375.3

AA65124 GM07265.3

AM540266 GH07625.3

AI518472 LD37996.3

BI337756 NCCSH8T3

CD866408 AZOZ. 0730

CD873121 AZOZ. 0730

CD873121 AZOZ. 1226

BMS84191 170006872

CC539904 CH240 420

AZ124708 OSJRBD007

CC849995 NDL.121H1

AQ91484 HD820409P

CK203195 FGAS01172

CK203195 FGAS01172

CK203195 FGAS01172

CK203537 FGAS01206

CA583063 EST000957

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CA583063 CK3COCKT

AZ264457 RPCI.23-4

BB589921 BB589921

BB604685 BB604685

AU06465 BB604685

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Surlactoroum uncatacous platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Juliangara, D. Bonaldo, M. L. Kitajima, J. P., Adamson, R. E., Ashton, P. D., Bonaldo, M. F., Kitajima, J. P., Adamson, R. E., Ashton, P. D., Bonaldo, M. F., Initon, G. P., Pariasol, L. C. C., Marques, R. C. P., Miyasato, P. P., Initon, G. P., Soares, M. B., Gargorio, S. P., Mysasto, P. M., Nascimento, A. L. T. O., Ohlweiler, F. P., Reis, E. M., Ribeiro, M. A., Satubal, J. C., Leite, L. C. Soares, M. B., Gargioni, C., Kawano, T., Setubal, J. C., Leite, L. C. C. and Dias-Neto, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD087130 42.0 bp mRNA linear BST 14-SEP-2003 MC1-0035T-R100-D10-U.G MC1-0035 Schistosoma mansoni cDNA clone MC1-0035T-R100-D10.G, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Dr. Sergio Verjovski-Almeida
                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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22879926
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CKZ03135
CKZ03537
CKZ681282
CAS81282
CAS81282
CNSO02EC
BUS98465
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BUS981902
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BY275272
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SOURCE
                                   CD087130 MC1-0035T
CG745724 P038-3-H1
B1936798 dC89d01.x
BE517377 WHE0625_B
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                                                              August 4, 2004, 05:41:25; Search time 1462.92 Seconds (without alignments) 428.668 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                          55026578
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                      27513289 segs, 14931090276 residues
                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Gapop_60.0 , Gapext 60.0
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Length 1128;

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95.2%;
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Unpublished (1997)
                                           Local Similarity 100 es 21; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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TITLE
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Pristionchus pacificus
Pristionchus pacificus
Pristionchus pacificus
Nedaryota, Metazoa, Nematoda, Chromadorea; Diplogasterida;
Neodiplogasteridae, Pristionchus.
1 (bases 1 to 1128)
Srinivasan, J., Sinza,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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                                                                              Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MC1-00357-R100 row: 10 column: D.
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="caxon:54126"
/clone_lib="Pax Bcorl BAC Library"
/note="The library was generated by a partial digest of the genemic DNA with Bcorl and cloning into the BAC vector."
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601491
Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOl. Genet. Genomics 269 (5), 715-722 (2003)
22835951
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/mol_type="genomic DNA"
/strain="California"
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|Jab host="Biomphalaria glabrata"
|clone lib="MCI-0035"
|note="Vector: pGEM T-easy"
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mol_type="mRNA"

db_xref="taxon:6183"

/clone="MC1-0035T-R100-D10.G"

/sex="mixed pool"
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Location/Qualifiers
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ORIGIN

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
   Tissue Produzement: Martha Rebbert, Steven L. Klein, Ph.D.
   Tissue Produzement: Martha Rebbert, Steven L. Klein, Ph.D.
   CDNA Library Preparation: Life Technologies, Inc.
   CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)
   DNA Sequencing by: Mashington University Genome Sequencing Center
   Clone distribution: Asnopus clones from this library are available
   through the I.M.A.G.B. Consortium/LML at: info@image.llnl.gov
   Trace considered overall poor quality
   Possible reversed clone: similarity on wrong strand
   Seq primer: -40UP from Gibco
   High quality sequence stop: 1.
   Location/Qualifiers
                                                                                                                                                                                                                                                                  dc89d01.x1 NICHD XGC CO1 Xenopus laevis cDNA clone IMAGE:3404257 3' similar to TR:014597 014597 NON-FUNCTIONAL FOLATE BINDING PROTEIN. 1, mRNA sequence.
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WHENGES BOG CIIZA Wheat ABA-treated embryo cDNA library Triticum aestivum cDNA clone WHENGES_B06_C11, mRNA sequence.
BES17377
BES17377.1 GI:9741407
Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:3404257"
/tissue_type="oocytes"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC OO1"
/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1;
Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Life Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
1 (bases 1 to 316)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                         Gaps
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                                                         Indels
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100.0%; Score 21; DB 29; 100.0%; Pred. No. 8.4;
                                                         Mismatches
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Xenopus laevis
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/mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                                                                  477 GIGCCAGCAGCAGCGGIAATA 497
                                                                                                            1 GTGCCAGCAGCAGCGGTAATA 21
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KEYWORDS
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ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

FEATURES

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/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol=min="HNI INSS"
/db xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="vector: pHOS1; Site:" BRE 1; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The V + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                               Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
MAN library
Seq primer: M13-Reverse
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB812595 SWWDmfCAV08B01SK Wuchereria bancrofti microfilaria cDNA (SAN95SjL-WDMf) Wuchereria bancrofti cDNA clone SWWDmfCAV08B01 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wuchereria bancrofti
Wuchereria bancrofti
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Chohocercidae; Wuchereria.
1 (bases 1 to 73)
Williams, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes expressed in microfilaria of Wuchereria bancrofti
Genes expressed in microfilaria of Wuchereria bancrofti
Unpublished (1996)
Contact: Swilliams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.7%; Score 18; DB 28; Length 915; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Wuchereria bancrofti"
/mol_type="mRNA"
/db_xref="taxon:6293"
                                                                                                                                                                                                                       High quality sequence start: 176
High quality sequence stop: 283.
Location/Qualifiers
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Seq primer: pBluescript SK.
Location/Qualifiers
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Conservative 0;
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Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
CB832595
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Matches 18; Conserv
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CB832595/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Olin Anderson
US Department of Apriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595873
Exa: 5105595818
Exa: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Clothech Matchmaker 3' AD primer.
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                    Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermarotyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermarotyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldae; Triticae.

Tobaces: Triticae; Triticum.

I (bases: 1 to 418)

Anderson, O. D., Chao, S., Han, P.S., Hsia, C.C., Johnson, R.R, Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L., Tong, J.C., Verhey, S.D. and Walker-Simmons, M.K.

The structure and function of the expressed portion of the wheat genomes - ABA-treated embryo library
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1 (bases 1 to 915)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HM1:NSS sheared DNA library

Unpublished (2000)
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Department of Eukaryotic Genomics
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Entamoeba histolytica
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RESULT 5 AZ677920/c DEFINITION

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EST 21-APR-2003 CDNA

Gaps ..

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68 GIGCCAGCAGCAGCGGI 84
                                                                                                                                                                                          Populus tremula
Populus tremula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: Ml3mp19; The cDNA library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 148)
Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                   Gaps
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AU010207 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc05561, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nis.go.jp.
                                                   'clone_lib="Wuchereria bancrofti microfilaria cDNA
                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe
Bukaryota, Pungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetacee,
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                            81.0%; Score 17; DB 14; Length 73; 100.0%; Pred. No. 3.9e+02; ive 0; Mismatches 0; Indels
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/mol_type="mRNA"
/strain="972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (fission yeast)
                  'dev_stage="microfilaria"
'lab_host="XL1-Blue MRF'"
clone="SWWbmfCAV08B01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4896"
/clone="spc05561"
/sex="h minus"
                                                                      L-WDMf)"
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Matches 17; Conservative
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Gaps

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0; Indels

GTGCCAGCAGCAGCGGT 17

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CK107208
252 bp mRNA linear BST 01-DBC-2003 UB49DPG02.5pR Populus active cambium cDNA library Populus tremula cDNA clone UB49DFG02 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 252)
Starky, F., Bhalerao, R.R., Unneberg, P., Segerman, B., Nilsson, P.,
Brunner, A. M., Campaa, L., Jonsson-Lindvall, J., Tandre, K.,
Strauss, S.H., Sundberg, B., Gustafsson, P., Uhlen, M., Bhalerao, R.P.,
Nilsson, O., Sandberg, G., Karlsson, J., Lundeberg, J. and Jansson, S.
A Populus EST resource for functional genomics
Unpublished (2003)
Chfar ESTs: UH99DFG02, UB49DFG02, 3pR
Contact: Bo Segerman
Umea Plant Science Center, Department of Plant Physiology
                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Malpighiales, Salicaceae, Saliceae, Populus.
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Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Active_cambium"
/clone_lib="Populus_active_cambium_cDNA_library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17; DB 14; Length 252;
Pred. No. 4.6e+02;
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Schizosaccharomyces pombe

    .252
    /organism="Populus tremula"
/mol_type="mRNA"

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Tel: +46 90 786 5279
Fax: +46 90 786 6575
Email: bo.segerman@plantphys.umu.se.
Location/Qualifiers
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/clone="UB49DPG02"
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Contact: Mitsucki Morimyo
                                                                                                                    CK107208.1 GI:38591533
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AU007074.1 GI:3343532
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1 (bases 1 to 413)
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Best Local Similarity 100.0
....hes 17; Conservative
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AW940266
524 bp mRNA linear EST 02-DEC-2003
GH07623.3prime GH Drosophila melanogaster head port2 brosophila
melanogaster cDNA clone GH07623 3 similar to CG5514: FBan0005514
GO:[] located on: 3R 98B2-98B2;: 08/12/2002, mRNA sequence.
AW940266
BST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diamence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798

Bmail: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu more T residues at the beginning of the sequence, this clone probably contains an inverted insert. The sequence has been trimmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="GM Drosophila melanogaster ovary BlueScript" /note="Organ: ovary; Vector: BlueScript SK; Site 1: BcoRI; Stte_2: XhoI; Constructed using Stratagene ZAP-cDNA Synthesis kit. Oligo dT-primed and directionally cloned at EcoRI and XhoI in BlueScript SK(+/-)"
                                                                                                                                                                                                                                                                          AA695154 GMO2326.3prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM02326 3prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
Drosophila melanogaster

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Bukaryota, Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 775)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Brock-HHMI Drosophila EST Project
Unpublished (2001)
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/lab_host="SOLR"
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81.0%; Score 17; DB 12; Length 460; 100.0%; Pred. No. 5e+02; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
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/organism="Drosophila melanogaster"
/moltype="mkNA"
/db xref="taxon;7227"
/clone="GM02326"
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High quality sequence stop: 406.
Location/Qualifiers
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                       Best Local Similarity 100.0%; P. Matches 17; Conservative 0;
                                                                                                                                                     156 TGCCAGCAGCAGCGTA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                       AA695154
     Query Match
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AW940266/c
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DEFINITION
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KEYWORDS
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic AE003763: arm:3R [23621985, 23825541]
                                                                                                                                                                                               /clone_lib="Schizosaccharomyces pombe late log phase cDNA" hote="Weetor: Ml3mpl9; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of Ml3mpl9 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
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/dev_stage="adult"
/lab_host="DH5 - alpha"
/lab_host="DH5 - alpha"
/lone lib="GH Drosophila melanogaster head pCT2"
/nore="Organ: head; Vector: pOT2; Site 1: EcRI; Site 2:
XhoI; Sized fractionated cDNAs were directly ligated Into
pOT2. Plasmid cDNA library."
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Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Neptora: Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neptora: Endopterygota, Diptera; Brachycera; Muscomorpha,
Ephydroidea, Drosophilae, Drosophila.

I bases 1 to 460)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubil, G.M.
DROSOphila EST Project
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                             l. .413
'organism="Schizosaccharomyces pombe"
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/organism="Drosophila melanogaster"
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Plate: GH.63 row: G column: 3
High quality sequence stop: 444.
Location/Qualifiers
                                                                                                                       /db_xref="taxon:4896"
/clone="spc01418"
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/db_xref="taxon:7227"
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  Location/Qualifiers
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Other_ESTs: GH06375.5prime
Contact: Stapleton, M.
                                                                       /mol_type="mRNA"
/strain="972"
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                             source
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nes 17; Conserv
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                                                                                                                                                                                                                                                                                         Distriction Rd, Berkeley, CA 94720, USA

Pax: 510 486 6798

Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu

Based upon the presence of a XhoI site followed by a run of 14 or

moreT residues at the beginning of the sequence, this clone was

polyadenylated. The resulting Poly-T sequence has been removed. hit

genomic AE003763: Drosophila melanogaster genomic scaffold
142000013386035 section 88 of 105, complete sequence.: 02/16/2001

High quality sequence stop: 382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIS18472 EST 19-APR-2001 LD37996.3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD37996 3prime, mRNA sequence.
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/lab_host="DHS - alpha"
/clone lib="GH Drosophila melanogaster head pOT2"
/clone lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhOI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
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Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 540)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,BDCP/HHMI Drosophila EST Project
Unpublished (2001)
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One Cyclotron Ed, Berkeley, CA 94720, USA
One Yels 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Braaryota, Metazooa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
I (Dases I to 534)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S., and Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'sex="male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                         Unpublished (2001)
Other ESTs: GH07623.5prime
Contact: Stapleton, M.
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100.0%; Pze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="GH07623"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 81.0
Best Local Similarity 100.
Matches 17; Conservative
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AI518472/c
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KEYWORDS
SOURCE
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             SOURCE
ORGANISM
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JOURNAL
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                         REFERENCE
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more T residues at the beginning of the sequence, this clone probably contains an inverted insert. The resulting Poly-T sequence has been removed.

Plate: 379 row: H column: 12

High quality sequence stop: 440.

Location/Qualifiers

1. 540

/organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Bukamalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 554)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunstein,A., deoliveira,P.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., Simpson,D.H., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                /sex="male and female"
//dev stage="0 to 24 hours mixed stage embryonic"
//dev stage="XL" Blue"
//clone lib="XL" Blue"
//clone lib="LD Drosophila melanogaster embryo pOT2"
//note="Organ: embryo; Vector: pOT2; Site 1: EcoRI; Site 2:
XhoI; Sized fractionated cDNAs were directly ligated into
POT2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF331275
RCS-BT0377-030200-012-G03 BT0377 Homo sapiens cDNA, mRNA sequence.
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Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC5&t2=RC5-BT0377-030200-012-G03&t3=2000-02-03&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 540;
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100.0%; Pred. No. 5.1e+02;
cive 0; Mismatches 0;
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High quality sequence start: 74
High quality sequence stop: 91.
Location/Qualifiers
1. 554
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="LD37996"
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/dev stage="germinating conidia"
/clone_lib="Conidial"
/note="mRNA isolated from germinating conidia, grown in lx Vogel's, 2% sucrose for 4.5 hours. cDNA directionally cloned into pBluescript SK(-) using the Uni-ZAP XR vector system (Stratagene, La Jolla, CA)."
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1 (bases I to 619)

Nelson, M.A., Kang, S., Braun, B.L., Crawford, M.E., Dolan, B.L., Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Blueyes, E., Cushing, T., Errett, A., Fleharty, M., Gorman, M., Judson, K., Miller, R., Ortega, J., Pavlova, I., Perea, J., Todisco, S., Trujillo, R., Valentine, J., Wells, A., Werner Washburne, M., Yazzie, S. and Natvig, D.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI397756 619 bp mRNA linear EST 08-FEB-1999 NCC5H8T3 Conidial Neurospora crassa cDNA clone NC5H8 5', mRNA
                     /note="Organ: breast; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressed sequences from conidial, mycelial, and sexual stages of Neurospora crassa
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Department of Biology
University of New Mexico
Castetrer Hall, Albuquerque, NM 87131, USA
Tel: 505 277 3411
Fax: 505 277 0304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Neurospora crassa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fungal Genet. Biol. 21, 348-363 (1997)
                                                                                                                                                                                                                                             Query Match

81.0%; Score 17; DB

Best Local Similarity 100.0%; Pred. No. 5.1

Matches 17; Conservative 0; Mismatches
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/strain="74-OR23-IV A"
/db_xref="taxon:5141"
/clone="NC5H8"
                                                                                                                                                                       stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Mating type A"
/tissue_type="Conidia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ngp@biology.unm.edu.
    Location/Qualifiers
    1. .619
clone lib="BT0377"
                                                                                                                                                                                                                                                                                                                                                  3 GCCAGCAGCAGCGGTAA 19
                                                                                                                                                                                                                                                                                                                                                                                     49 GCCAGCAGCAGCGGTAA 33
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BST.
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AI397756/c
LOCUS
DEFINITION
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KEYWORDS
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MEDLINE
PUBMED
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AUTHORS
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Gaps

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Query Match

81.0%; Score 17; DB 9; Length 619;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels

1 GTGCCAGCAGCGGT 17

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279 GTGCCAGCAGCAGT 263
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Search completed: August 4, 2004, 09:20:58 Job time : 1466.92 secs

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Sequence 4, Appli
Sequence 5583, Ap
Sequence 5383, Ap
Sequence 5385, Ap
Sequence 27485, A
Sequence 12478, A
Sequence 12478, A
Sequence 12478, A
Sequence 12478, Ap
Sequence 166711,
Sequence 166711,
Sequence 166711,
Sequence 16711,
Sequence 2841, Ap
Sequence 2841, Ap
Sequence 602, Ap
Sequence 10712, A
Sequence 10712, A
Sequence 20052, A
Sequence 10712, A
Sequence 1032, A
Sequence 20052, A
Sequence 1032, A
Sequence 1032, A
Sequence 1032, A
Sequence 1032, A
Sequence 10321, A
Sequence 10321, A
                                                                     August 4, 2004, 06:43:54 ; Search time 218.94 Seconds (without alignments) 247.629 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                             Pending Patents NA New:*

1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
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9: /cgn2_6/ptodata/2/pna/USIO_NEW_COMB.seq2:*
                                                                                                                                                                                                                                                                         9508132
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-729-961-4
US-10-729-961-1
US-09-40-520B-583
US-10-896-891-531
US-10-100-683-3306
US-09-248-796A-35733
US-10-767-701-12478
US-09-404-520B-20466
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US-10-100-683-13121
US-10-745-444-764
US-10-745-741-10712
US-10-748-333A-600711
US-10-843-527-119324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                   nucleic search, using sw model
                                                                                                                          US-09-940-860-3
22
1 acaaggcccgagaacgtattca 22
                                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                                                                                                                                               OLIGO_NUC
Gapop_60.0 , Gapext 60.0
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length: 2000000000
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RESULT 1

US-10-729-961-4/C

Sequence 4, Application US/10729961

Sequence 4, Application US/10729961

Sequence 4, Application US/10729961

Sequence 4, Application US/10729961

APPLICANT: ITANO, Worthide

APPLICANT: YANO, Yoshitaka

TITLE OF INVENTION: For Detecting Fusobacterium Nucleatum By Pcr Methods And

TITLE OF INVENTION: Por Detection

FILE REPERBRICE: 246312080

CURRENT APPLICATION NUMBER: US/10/729,961

CURRENT PILING DATE: 2003-12-09

PRIOR PILING DATE: 2002-12-10

PRIOR FILING DATE: 2003-12-02

PRIOR FILING DATE: 2003-12-02

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Version 3.1
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GENERAL INFORMATION:
APPLICANT: INASE, Tadayuki
APPLICANT: INASE, Tadayuki
APPLICANT: ITANO, Morihide
APPLICANT: TANO, Poshitaka
TITLE OF INVENTION: Primers For Detecting Fusobacterium Nucleatum By Pcr Methods And
TITLE OF INVENTION: For Detection
FILE REFERENCE: 246312US0
CURRENT APPLICATION NUMBER: US/10/729,961
CURRENT FILING DATE: 2003-12-09
PRIOR APPLICATION NUMBER: JP 2002-388698
PRIOR FILING DATE: 2002-12-10
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Sequence 36908, A Sequence 213, Ap Sequence 2213, Ap Sequence 2213, Ap Sequence 22147, Ap Sequence 2646, A Sequence 26196, A Sequence 26196, A Sequence 26196, A Sequence 26196, A Sequence 28589, A Sequence 9569, Ap Sequence 9569, Ap Sequence 9569, Ap Sequence 9569, Ap Sequence 2882, Ap Sequence 26134, App Sequence 164349, Ap Sequence 164349, Sequence 1635, Ap
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US-09-404-520B-36908

US-60-579-902-11666

US-60-579-902-1213

US-60-579-662-2213

US-10-425-115-20380

US-10-834-987-2447

US-10-834-987-2447

US-09-404-520B-26196

US-09-404-520B-26196

US-09-404-520B-26196

US-10-425-115-108619

US-10-896-891-9569

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Pred. No. 0.47;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.7%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Fusobacterium nucleatum
US-10-729-961-4
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Matches 16; Conserv
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US-10-729-961-1/c
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        SEQ ID NO 4
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Query Match
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APPLICANT: Hinke, Gregory J.
APPLICANT: Hinke, Gregory J.
APPLICANT: Hinke, Gregory J.
APPLICANT: McIninch, James
APPLICANT: McIninch, James
APPLICANT: McIninch, Jacia
TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/404,520B
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 44345
SEQ ID NO 5583
LENGTH: 8004
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GENERAL INFORMATION:
BPPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CANCER, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH CANCER, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOOT/88
CURRENT PAPLICATION NUMBER: 05/10/896,891
CURRENT FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: 60/231,328
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 12618
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                            NAME/KEY: misc_feature
i_LOCATION: (1650)..(1650)
i_CTHER_INFORMATION: n stands for any base
0S-10-729-961-1
PRIOR APPLICATION NUMBER: JP 2003-403715
PRIOR FILING DATE: 2003-12-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1661
TYPE: DNA
ORGANISM: Fusobacterium nucleatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
2.09-404-520B-5583/C
3.Sequence 5583, Application US/09404520B
GENERAL INFORMATION:
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Best Local Similarity
Matches 16; Conservat
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US-10-896-891-531/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OKGANISM: EMELLY
US-09-404-520B-5583
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; ORGANISM: Human
US-10-896-891-531
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LENGTH: 281443
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Wis-0s-40-520B-27485

Sequence 27485, Application US/09404520B

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Tamberlake, William E.
APPLICANT: Timberlake, William E.
APPLICANT: Timberlake, William E.
APPLICANT: Timberlake, James
APPLICANT: Yu, Jaehyuk
APPLICANT: Yu, Jaehyuk
TITLE OF INVERTION: Emericella nidulans Genome Sequence and Uses Thereof
TITLE OF INVERTION: Emericella nidulans Genome Sequence and Uses Thereof
TITLE REPRENCE: 38-10(15498) A
CURRENT APPLICATION NUMBER: US/09/404,520B

CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 27485
LENGTH: 1080
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NUMBER OF SEQ ID NOS: 13468
SOFTWARE: Patentin Ver. 2.0
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68.2%; Score 15; DB 6; Length 281443; 100.0%; Pred. No. 2.9;
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100.0%; Pred. No. 10;
iive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAIN SECTECED FIGURISMS
TITLE OF INVENTION: HUMAIN SECTECED FIGURISMS
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
PRIOR FILING DATE: 1997-03-07
PRIOR PELING DATE: 1997-04-11
PRIOR FILING DATE: 1997-04-11
PRIOR FILING DATE: 1997-06-23
PRIOR PELING DATE: 1997-06-21
PRIOR PELING DATE: 1997-06-22
PRIOR PELING DATE: 1997-06-22
PRIOR APPLICATION NUMBER: US 60/043,580
PRIOR PELING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/043,580
PRIOR PELING DATE: 1997-04-11
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 Human Secreted Proteins
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; Sequence 3306, Application US/10100683
; GENERAL INFORMATION:
         68.20;
100.0%; Pre
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Best Local Similarity 100.
Matches 14; Conservative
                                                            Conservative
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CORGANISM: Homo sapiens
US-10-100-683-3306
                           Best_Local Similarity
Matches 15; Conserv
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thous K.
APPLICANT: ADou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
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                                                                                APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Tinberlake, William E.
APPLICANT: McIninch, James
APPLICANT: Yu, Jaehyuk
APPLICANT: Yu, Jaehyuk
APPLICANT: Woldssi, Azita
TITLE OF INVENTION: Emerical nidulans Genome Sequence and Uses Thereof
FILE REFERENCE: 38-10 (15498)A
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 44345
SEQ ID NO 9481
LENGTH: 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Tinberlake, William E.
APPLICANT: McIninch, James
APPLICANT: Yu, Jaehyuk
APPLICANT: Yu, Jaehyuk
APPLICANT: Yu, Jaehyuk
APPLICANT: Yu, Jaehyuk
APPLICANT: AZita
ITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
FILE REPERBNCE: 38-10(15498)A
CURRENT APPLICATION NUMBER: US/09/404,520B
NUMBER OF SEQ ID NOS: 44345
SEQ ID NO 20466
LENGTH: 1389
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red. No. 10;
Mismatches 0
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; Sequence 20466, Application US/09404520B
; GENERAL INFORMATION:
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// GENERAL INFORMATION:
                   US-09-404-520B-9481
; Sequence 9481, Application US/09404520B
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pr
Matches 14; Conservative 0;
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Best Local Similarity 100.0%;
Matches 14; Conservative 0
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ORGANISM: Emericella nidulans
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
RECOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 3573
LENGTH: 1215
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US-10-76-701-12478

Sequence 12478, Application US/10767701

Sequence 12478, Application US/10767701

Sequence 12478, Application US/10767701

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yinds

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT PLING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 12478

LENGTH: 1271
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                                                                                          DB 5; Length 1080;
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US-10-767-701-12478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
10;
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10;
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Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches
                                                                                       Query Match 63.6%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 10, Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                           Sequence 3573, Application US/09248796A GENERAL INFORMATION:
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100.0%; Pre
TYPE: DNA ORGANISM: Emericella nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1151 ACAAGGCCCGAGAA 1164
                                                                                                                                                                                                                             904 CGAGAACGTATTCA 917
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Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA; Candida albicans US-09-248-796A-3573
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                                           US-09-404-520B-27485
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US-10-501-933-4270
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LENGTH: 2307
                                                                                                                                                                                                                       TYPE: DNA
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Matches
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Sequence 14910. Application US/09404520B

Sequence 14910. Application US/09404520B

APPLICANT: Cao, Yongwei

APPLICANT: Timberlake, William E.

APPLICANT: Timberlake, William E.

APPLICANT: McInich, James

TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof

FILE REFERENCE: 38-10[15499]

CURRENT APPLICATION NUMBER: US/09/404,520B

CURRENT FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 44345

SEQ ID NO 14910

LENGTH: 1866
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Pred. No. 11;
0; Mismatches 0; Indels
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Pred. No. 10;
                                                                                                                                                                                                                                                                      0; Indels
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CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
RIOR APPLICATION NUMBER: US 60/040,162
PRIOR PILING DATE: 1997-03-07
PRIOR FILING DATE: 1997-04-11
PRIOR FILING DATE: 1997-04-11
PRIOR PAPLICATION NUMBER: US 60/043,576
PRIOR APPLICATION NUMBER: US 60/043,601
PRIOR FILING DATE: 1997-04-11
PRIOR FILING DATE: 1997-04-12
PRIOR FILING DATE: 1997-04-22
PRIOR FILING DATE: 1997-04-23
PRIOR FILING DATE: 1997-04-23
PRIOR FILING DATE: 1997-04-23
PRIOR FILING DATE: 1997-04-11
PRIOR FILING DATE: 1997-04-13
PRIOR FILING DATE: 1997-04-12
                                                                                                                                                 ; OTHER INFORMATION: Clone ID: MRT4577_83619C.1
US-10-425-115-166711
                                                                                                                                                                                                                       Query Match 63.6%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 10; Matches 14; Conservative 0; Mismatches
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Sequence 2841, Application US/10100683
GENERAL INFORMATION:
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Conservative 0;
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US-09-404-520B-14910
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NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 166711
LENGTH: 1553
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Best Local Similarity
                                                                           TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                         FEATURE:
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APPLICANT: 141, Preet;
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Bughn, Mariah R.
APPLICANT: Shah, Purvi
CURRENT SPERENCE: PA-0017 US
CURRENT APPLICATION NUMBER: US/10/745,444
ANNUMBER OF SEQ ID NOS: 809
SOFTWARE: PERL Program
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PRIOR APPLICATION NUMBER: US 60/047,632
PRIOR FILING DATE: 1997-05-23
PRIOR FILING DATE: 1997-06-82
PRIOR FILING DATE: 1997-06-82
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 13468
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2841
LENGTH: 1959
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Pred. No. 11;
0; Mismatches 0; Indels
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Pred. No. 11;
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APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Gene Logic, Inc.
TILE REPERENCE: 44921-5038-01-00
CURRENT FILING DATE: 2004-07-20
CURRENT FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR PILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.6%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 11; Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature; OTHER INPORMATION: Incyte ID NO: 1997168CT1: PUBLICATION INFORMATION: US-10-745-444-764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4270, Application US/10501933 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 764, Application US/10745444 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 63.6%; SCOL
100.0%; Pre
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                                                                                                                                                                                                                                                       , ORGANISM: Homo sapiens
US-10-100-683-2841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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hes 14; Conserval
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PRIOR FILING DATE: 2000-11-02
PRIOR PLICATION NUMBER: US 60/290,029
PRIOR PLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-15
PRIOR PLING DATE: 2001-06-06
PRIOR PLING DATE: 2001-06-06
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-07-09
PRIOR PLING DATE: 2001-0
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CRGANISM: Rattus norvegicus
FEATURE:
COMBANISM: Restus norvegicus
COMBANISM: Restus Norvegicus
COMBANISM:
COMBANISM: Genbank Accession No. X83231
US-10-501-933-4270
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Search completed: August 4, 2004, 11:43:46 Job time : 220.94 secs

1128 ACAAGGCCCGAGAA 1141

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August 4, 2004, 06:32:11 ; Search time 2008.36 Seconds (without alignments) 385.436 Million cell updates/sec
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| cgn12 | cfptcdata/2/pna/USO8 | comB.seq:* |
| cgn12 | cfptcdata/2/
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2004
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                                                                                             OM nucleic - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Word size
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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100.0%; Score 22; DB 39; ilarity 100.0%; Pred. No. 0.0095; Conservative 0; Mismatches 0;

Query Match Best Local Similarity Matches 22; Conservat

Length 22;

; OTHER INFORMATION: synthetic amplification primer US-09-940-860-3

RESULT 1	US-U9-94U-86U-3	Sequence 3, Application US/09940860	GENERAL INFORMATION:	APPLICANT: Rothman, Richard	APPLICANT: Majmudar, Maulik	TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF	FILE REFERENCE: 01107.00185	CURRENT APPLICATION NUMBER: US/09/940,860	CURRENT FILING DATE: 2001-08-29	PRIOR APPLICATION NUMBER: 60/229,376	PRIOR FILING DATE: 2000-08-31	NUMBER OF SEQ ID NOS: 7	SOFTWARE: FastSEQ for Windows Version 4.0	SEQ ID NO 3	LENGTH: 22	. TYPE: DNA	ORGANISM: Artificial Sequence	FEATURE:	**	
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Sequence 2, Appli
Sequence 36, Appl
Sequence 15, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 2, Appl
Sequence 1, Appli
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                                                                                                                                                                                                                                                                                                                   Sequence 4,
Sequence 5,
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Sequence 3,
Sequence 3,
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Sequence 7,
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Sequence 2,
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Sequence 6
Sequence 2
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                    Description
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                                                                          PCT-USO1-116 030A-2
PCT-USO1-116 030A-2
PCT-USO3-1-16 030A-2
US-07-923-871B-36
US-07-9248-998E-7
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100.0 1451
100.0 11621
100.0 116217
100.0 910715
100.0 1230025
100.0 1230230
100.0 1230230
95.5 1538230
                    Length
Query
                                                                                                                                              100.0
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### T.TGNMENTS

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Sequence 2, Application PC/TUS0303202
Sequence 2, Application PC/TUS0303202
Sequence 2, Application PC/TUS0303202
Sequence 2, Application PC/TUS0303202
SEQUENCE 1NFORMATION: Application of Microbial Dechlorination of Polychlorinated Biphen TITLE OF INVENTION: Halogenated Ethenes
FILE REFERENCE: 4115-176 PCT
CURRENT APPLICATION NUMBER: PCT/US03/03202
CURRENT FILING DATE: 2002-02-03
PRIOR APPLICATION NUMBER: 60/353,134
PRIOR APPLICATION NUMBER: 60/353,134
PRIOR APPLICATION NUMBER: 60/353,134
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 336
TYPE: DNA
CRENTSH: Artificial Sequence
                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sowers, Kevin R.
APPLICANT: Sowers, Kevin R.
APPLICANT: Sowers, Kevin R.
APPLICANT: May, Harchid D.
TITLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of Polychlo TITLE OF INVENTION: Empheryl Compounds
FILE REFERENCE: 4115-149 PCT
CURRENT FILING DATE: 2001-05-18
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 3
SEQ ID NOS: 3
SEQ ID NO 2
LENGTH: 336
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; OTHER INFORMATION: Synthetic Construct
PCT-US03-03202-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
) OTHER INFORMATION: Synthetic construct
PCT-US01-16030A-2
RESULT 2
PCT-US01-16030A-2/c
; Sequence 2, Application PC/TUS0116030A
; GENERAL INFORMATION:
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 ACAAGGCCCGAGAACGTATTCA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 22; Conservative
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PCT-US03-03202-2/c
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Gaps
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GENERAL INFORMATION:
APPLICANT: White Ph.D. Thomas J.
APPLICANT: Dodge, Deborah E.
TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-923-871B-35/c

Sequence 35, Application US/07923871B

GENERAL INFORMATION:

APPLICANT: White Ph.D, Thomas J.

APPLICANT: Dodge, Deborah E.

TITLE OF INVENTION: Method for Diagnosis of Lyme Disease

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESES: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110-1199
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,871B
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,871B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8697
TELECOMMUNICATION INFORMATION:
TELECHNUM: (50,0),10,10,10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 acaaggcccgagaaccrarrca 252
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                      340 Kingsland Street
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (510) 814-2977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 368 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 07110-1199
                                                                                                                                                                                                               Nutley
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                                                                                                                                                                                   Sequence 2, Application PC/TUS0303202A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of Maryland Biotechnology Institute
APPLICANT: University of Maryland Biotechnology Institute
APPLICANT: University of Microbial Dechlorination of Polychlorinated Bipher
TITLE OF INVENTION: Stimulation of Microbial Dechlorination of Polychlorinated Bipher
TITLE OF INVENTION: Halogenated Ethenes
FILE REFERENCE: 4115-176 PCT
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: 60/353,134
PRIOR APPLICATION NUMBER: 60/353,134
PRIOR PILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

Sequence 2, Application US/09860200D

GENERAL INFORMATION:

APPLICANT: Kevin, Bowers R.

APPLICANT: Harold, May D.

TITLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of TITLE OF INVENTION: Oppositions and Methods for Microbial Dechlorination of TITLE OF INVENTION: Oppositions and Methods for Microbial Dechlorination of TITLE OF INVENTION: Oppositions and Methods for Microbial Dechlorination of TITLE OF INVENTION: Opposition of STILE REFERENCE: 4115-149

CURRENT FILING DATE: 2003-02-20

PRIOR PLICATION NUMBER: US 60/266,650

PRIOR FILING DATE: 2001-02-06

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 336
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100.0%; Score 22; DB 35; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 22; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Synthetic Construct PCT-US03-03202A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Synthetic Construct US-09-860-200D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 ACAAGGCCCGAGAACGTATTCA 302
                                                        323 ACAAGGCCCGAGAACGTATTCA 302
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US-07-923-871B-36/c
; Sequence 36, Application US/07923871B
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ORGANISM: Artificial Sequence
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                                                                                                                                                             -US03-03202A-2/c
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LENGTH: 336
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07923871
GENERAL INFORMATION:
APPLICANT: White Ph.D, Thomas J.
APPLICANT: Odde, Deborah E.
TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADGRESSEE: ADGRESSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/923,871

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION TAN:

APPLICATION TOWER: US/07/923,871

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION TAN:

APPLICATION NUMBER: US/050

ATTORNEY/AGRYT INFORMATION:

REGISTRATION NUMBER: 32,630

REGISTRATION NUMBER: 8697

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 114-2863
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ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ACAAGGCCCGAGAACGTATTCA 22
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                                                                                                        complement (35..36)
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SEQUENCE CHARACTERISTICS:
LENGTH: 505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
FEATURE:
NAME/KEY:
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FEATURE:
NAME/KEY:
LOCATION:
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; LOCATION:
US-07-923-871B-1
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STATE:
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Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 22; Conservative 0; Mismatches 0; Indels
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US-07-923-871B-1/C
Sequence 1, Application US/07923871B
Sequence 1, Application US/07923871B
Sequence 1, Application US/07923871B
SEPELICANT: White Ph.D, Thomas J.
APPLICANT: Makeholis Photon Disease
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: ADGRESSE:
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NUT
COUNTRY: USA
ZUP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEBLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,871B
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A:
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8697
TELEPHONE: (510) 814-2974
TELEPHONE: (510) 814-2974
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CLAUSE TEATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Perry, DOUGJAS A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8697
TELEPHONE: (510) 814-2974
TELEPHONE: (510) 814-2977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 ACAAGGCCCGAGAACGTATTCA 254
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                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 35: SEQUENCE CHARACTERISTICS: LENGTH: 370 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO: 1:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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Sequence 94, Application US/10061071
Sequence 94, Application US/10061071
APPLICANT: B.I. DUPONT DE NEMOURS & COMPANY
APPLICANT: HINDRICKSON, EDWIN
TITLE OF INVENTION NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION: BACTERIA
FILE REFERENCE: BC1002 US CIP
CURRENT FILING DATE: 1099-04-15
PRIOR APPLICATION NUMBER: US 60/129,511
PRIOR APPLICATION NUMBER: G0/129,511
PRIOR APPLICATION NUMBER: 60/129,511
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
SEQ ID NO 94
SEQ ID NO 94
TENDER PILING DATE: 1099-04-15
IENGTH 1014
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APPLICANT: Ebersole, Richard C.
APPLICANT: Hendrickson, Edwin
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION: BACTERIA
FILE REPERBNCE: BCI002 US NA
CURRENT APPLICATION NUMBER: US(09/548,998A
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 22; DB 3; Length 50; Pred. No. 0.0074; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Dehalococcoides related Family A Group US-10-061-071-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 ACAAGGCCCGAGAACGTATTCA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1004 ACAAGGCCCGAGAACGIATICA 983
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; Sequence 2, Application US/09548998A
; GENERAL INFORMATION:
                                                                      complement (35..36)
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Best Local Similarity 100.0%;
Matches 22; Conservative 0,
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ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                     complement (167)
                                                                                                                                                                                                                                                                                                                                                                                                                                         unsure
complement (169)
                                                                                                                                                                                                                             (67)
                                                                                                                                                      complement
                                                                                                                                                                                                         unsure
complement
                                                                                                                                                                                                                                                                                                            complement
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Best Local Similarity
                                                      unsure
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                                                                                                                                                                                                                                                                                      unsure
                                                                                                                                                                                                                                                                                                                                                               unsure
ANTI-SENSE:
FEATURE:
NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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LOCATION:
FEATURE:
                                                                                                                                                                         FEATURE:
NAME/KEY:
LOCATION:
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; LOCATION:
US-07-923-871A-1
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APPLICANT: White Ph.D, Thomas J.
APPLICANT: Dodge, Deborah E.
TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
NUMBER OF SEQUENCE: 30
CORRESPONDENCE ADDRESS:
ADDRESSES: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTY: USA
ZIP: O7110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTRATING SYSTEM: PC-DOS/MS-DOS
SOFTRATING SYSTEM: US/07/923,871A
APPLICATION NUMBER: US/07/923,871A
FILING DATE:
CLASSIFICATION NUMBER: US/07/923,871A
FILING DATE: TO-MAR-1990
ATPONITY/AGENT INFORMATION:
NAME: Sias, Stace R.
TELECOMUNICATION INPERE: 32,630
REGISTRALICATION NUMBER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 22; DB 3; Length 505; 100.0%; Pred. No. 0.0074; Pred. D. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 ACAAGGCCCGAGAACGTATTCA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-923-871A-1/c
; Sequence 1, Application US/07923871A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              complement (164..165)
                                                                               complement (35..36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                        complement (167)
                                                                                                                                                                                                                                                                                                                                                                                                                                            unsure
complement (169)
                                                                                                                                                                                                                                  complement (67)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 22; Conservative
                                                         unsure
                                                                                                                                  unsure
                                                                                                                                                                                                            unsure
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                                                                                                                                                                                                                                                                                                                                                                  unsure
                                                                            LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
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LOCATION:
FEATURE:
  ANTI-SENSE:
FEATURE:
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, LOCATION:
US-07-923-871-1
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FEATURE:
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Search completed: August
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US-09-548-998A-6/c
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APPLICANT: Ebersole, Richard C.
APPLICANT: Ebersole, Boxin
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION: BACTERIA
FILE DEFINITION NUMBER: US/09/548,998A
CURRENT APPLICATION NUMBER: 00/129-10
FRIOR PRILICATION NUMBER: 60/129-511
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: MICLOSOft Office 97
SEQ ID NO 5
ILBNGTH: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bersola.
APPLICANT: Bersola.
TITLE OF INVENTION : BACTERIA
TITLE OF INVENTION : WICLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION : WICLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION : BACTERIA
TITLE OF INVENTION : BACTERIA
TITLE OF INVENTION : BACTERIA
CURRENT APPLICATION NUMBER: US/09/548,998A
CURRENT APPLICATION NUMBER: 60/129,511
PRIOR PLING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
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100.0%; Score 22; DB 23; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 22; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/129,511
PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Dehalococcoides ethenogenes
                                                                                                                                                                                                                                                                                                                                                                                                                            1321 ACAAGGCCCGAGAACGTATTCA 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Dehalococcoides ethenogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1321 ACAAGGCCCGAGAACGTATTCA 1300
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; ORGANISM: Dehalococcoides ethenogenes
US-09-548-998A-5
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US-09-548-998A-4/C
                                                                                                                                                                                                               US-09-548-998A-2
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APPLICANT: Ebersole, Richard C.
APPLICANT: Bersole, Richard C.
APPLICANT: Bensole, Richard C.
APPLICANT: Bensole, Richard C.
APPLICANT: Hendrickson, Edwin
TITLE OF INVENTION: BACTERIA
TITLE OF INVENTION: BACTERIA
FILE OF INVENTION: BACTERIA
CURRENT APPLICATION NUMBER: US/09/548,998A
CURRENT FILING DATE: 1999-04-15
RIOR APPLICATION NUMBER: 60/129,511
PRIOR FILING DATE: 1999-04-15
NUMBER: OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4, 2004, 11:29:58
1321 ACAAGGCCCGAGAACGTATTCA 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; ORGANISM: Dehalococcoides ethenogenes US-09-548-998A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                                                           Sequence 6, Application US/09548998A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 22; Conservative
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August 4, 2004, 07:44:29 ; Search time 199.06 Seconds (without alignments) 541.892 Million cell updates/sec Published Applications Nat.

(gdn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
(cgn2\_6/ptodata/2/pubpna/US06\_PUBW\_PUB.seq:\*
(cgn2\_6/ptodata/2/pubpna/US06\_PUBW\_PUB.seq:\*
(cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
(cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
(cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
(cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
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(cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
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(cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
(cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\* GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. Total number of hits satisfying chosen parameters: 3222919 segs, 2451570024 residues Post-processing: Listing first 45 summaries OM nucleic - nucleic search, using sw model 1 acaaggcccgagaacgtattca 22 Gapop\_60.0 , Gapext 60.0 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 US-09-940-860-3 22 Published OFIGO NUC 0 Scoring table: Perfect score: Word size : Database : Sequence: Searched: Run on: Title:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 3, Appli	Sequence 2, Appli	Sequence 94, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 6, Appli	Sequence 3, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 16, Appl	Sequence 17, Appl	Sequence 18, Appl	Semience 1. Appli
ΔΙ	US-09-940-860-3	US-09-860-200D-2	US-10-061-071-94	US-10-061-071-2	US-10-061-071-4	US-10-061-071-5	US-10-061-071-6	US-10-061-071-3	US-10-061-071-7	US-10-289-762-1	US-10-391-249-16	US-10-391-249-17	US-10-391-249-18	115-10-053-078-1
<u>e</u>	11	10	15	12	15	15	15	15	75	16	11	11	17	4
% Query Match Length DB	22	336	1014	1377	1377	1377	1377	1378	1443	1230025	244	354	354	683
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0			72.7	72.7	72 7
Score	22	22	22	22	22	22	22	22	22	22	16	16	16	3.6
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Sequence 2, Appli Sequence 95, Appl	Sequence 1, Appli Sequence 1, Appli	54	67	23	22	93	(A	Sequence 2999, Ap	227,	38	œ	2320	e 11	Ĩ	Sequence 118, App	300	e 4089	4000,	e 9371,	817,	4000,	3999,	9370,	816	3999,	739	equence 1255,	H
-10-053-078- -10-061-071-	10-205-	-10-087-1	-10-040-739-6	-10-393-840-23	-10-393-840-22	-09-918-995-3222	-995-26	-10-066-543-29	-840-22	US-09-918-995-38009	US-09-942-025-8	US-09-974-300-2328	-09-933-767-11	-004-860-1	US-10-023-282-118	-425-114-3	93-40	US-09-764-877-4000	σ	-428-8	5-10-242-51	US-09-764-877-3999	9-764-891-93	-10-205-428-	-10-242-515-39	US-10-017-161-739	-10-087-192-12	US-09-942-025-1
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1385	105184 580073	238484	~	417	450	457	460	472	506	511	942	1032	101	1071	1071	1443	1602	5469	5469	5469	5469	9453	9453	9453	9453	35178	46675	67311
72.7	72.7					63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6		63.6				63.6		63.6
9 7 7	9 T P	15	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14
15	13	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

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Gaps
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US-09-940-860-3
| Sequence 3, Application US/09940860|
| Sequence 3, Application US/09940860|
| Publication No. US2004000555A1|
| GENERAL INFORMATION:
| APPLICANT: Rothman, Richard |
| APPLICANT: Majmudar, Maulik |
| TITLE OF INVENTION: WOLECULAR DIAGNOSIS OF BACTEREMIA |
| FILE REFERENCE: 01107.00185 |
| CURRENT FILING DATE: 2001-08-29 |
| PRIOR RIPLICATION NUMBER: 60/229,376 |
| PRIOR FILING DATE: 2000-08-31 |
| NUMBER OF SEQ ID NOS: 7 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NOS: 7 |
| SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 22; DB 11; Best Local Similarity 100.0%; Pred. No. 0.00054; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CIHER INFORMATION: synthetic amplification primer US-09-940-860-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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22 1 ACAAGGCCCGAGAACGTATTCA 22 1 ACAAGGCCCGAGAACGTATTCA ò g

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RESULT 2
US-09-860-200D-2/c
), Sequence 2, Application US/09860200D
; Publication No. US20030134408A1
; GENERAL INFORMATION:

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100.0%; Score 22; DB 15; 100.0%; Pred. No. 0.00045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
P. ORGANISM: Dehalococcoides ethenogenes strain PL
US-10-061-071-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                      CURRENT APPLICATION NUMBER: US/10/061,071
CURRENT FILING DAFE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/129,511
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION WUMBER: 60/129,511
PRIOR PILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 103
SOFTWARE: MICROSOFT Office 97
SEQ ID NOS: 13377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1321 ACAAGGCCCGAGAACGTATTCA 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Matches 22, Conservative
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NUMBER OF SEQ ID NOS: 103
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Best Local Similarity
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Sequence 94, Application US/10061071

Sequence 94, Application US/10061071

Sequence 94, Application US/10061071

Sequence 94, Application No. US20030077601A1

Sequence 94, Application No. US20030077601A1

Septicant: Bill Dupont De Nemours & COMPANY

APPLICANT: Bill DUPONT DE NEMOURS & COMPANY

TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING

TITLE OF INVENTION: BACTERIA

FILL REFERENCE: BC1002 US CIP

CURRENT APPLICATION NUMBER: US 60/129,511

PRIOR FILLING DATE: 1999-04-15

PRIOR FILLING DATE: 1999-04-15

NUMBER OF SEQ ID NOS: 103

SOFTWARE: Microsoft Office 97

SEQ ID NO 94
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| Publication No. US20030077601A1
| CENEAL INPOWERTION |
| APPLICANT: B.I. DUPONT BE NEMOURS & COMPANY |
| APPLICANT: HENDRICKSON, EDMIN |
| TITLE OF INVENTION: BACTERIA |
| FILE REFERENCE: BC1002 US CIP
APPLICANT: Kevin, Bowers R.

APPLICANT: Harold, May D.

TITLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of
TITLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of
TITLE OF INVENTION: Polychlorinated Biphenyl Compounds
FILE REFERENCE: 415-149
CURRENT APPLICATION NUMBER: US/09/860,200D
CURRENT FILING DATE: 2000-02-19
PRIOR APPLICATION NUMBER: US 60/265,818
PRIOR APPLICATION NUMBER: US 60/266,650
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
LEAGTH: 336
LEAGTH: MAINTENTINE LEAGTH:
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100.0%; Score 22; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 22; Conservative 0; Mismatches 0;
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, ORGANISM: Dehalococcoides related Family A Group
US-10-061-071-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Synthetic Construct US-09-860-200D-2
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 22; Conserva
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Sequence 4, Application US/10061071

Sequence 4, Application US/10061071

Publication No. US20030077601A1

GENERAL INFORMATION:

JAPLICANT: B.I. DUPONT DE NEMOURS & COMPANY

APPLICANT: HENRICKSON, EDWIN

TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING

TITLE OF INVENTION: NUMBER: US/10/061,071

CURRENT FILING DATE: 2002-01-29

FRIOR RPLING DATE: 1999-04-15

PRIOR PLING DATE: 1999-04-15

PRIOR PLING DATE: 1999-04-15

NUMBER OF SEQ ID NOS: 103

SEQ ID NO 4

LENGTH 13377

ENEMAL 13377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
APPLICANT: HENDRICKSON, EDWIN
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION: BACTERIA
FILE REFERENCE: BC1002 US CIP
CURRENT APPLICATION NUMBER: US/10/061,071
CURRENT FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
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Length 1377;
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100.0%; Pred. No. 0.00045;
tive 0; Mismatches 0;
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Sequence 7, Application US/10061071
; Sequence 7, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
    APPLICANT: B.I. DUPONT DE NEMOURS & COMPANY
APPLICANT: HENDRICKSON, EDWIN
; TITLE OF INVENTION: UDCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
; TITLE OF INVENTION: UDCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
; TITLE OF INVENTION: UDMER: US/10/061,071
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US 60/129,511
; PRIOR APPLICATION NUMBER: 60/129,511
; PRIOR FILING DATE: 1999-04-15
; PRIOR FILING DATE: 1999-04-15
; RIOR RILING DATE: 1999-04-15
; SOFTWARE: Microsoft Office 97
; SEQ ID NOS: 103
; SOFTWARE: Microsoft Office 97
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US-10-289-762-1/c
US-10-289-762-1/c
Sequence 1, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT: Griffals, R.
APPLICANT: Griffals, R.
APPLICANT: Griffals, R.
APPLICANT: Griffals, R.
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, previring PRERENCE: 9710-003-999
TITLE REPERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
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Length 1378;
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; Score 22; DB 15;
; Pred. No. 0.00045;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Dehalococcoides ethenogenes strain 195
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LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or g or
FEATURE:
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OTHER INFORMATION: n=a or c or g or
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   Query Match
Best Local Similarity 100.0%;
Matches 22; Conservative 0
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LOCATION: (1353)..(1353)
OTHER INFORMATION: N= unknown
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Matches 22, Conserv
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Sequence 6, Application US/10061071

Sequence 6, Application US/10061071

Publication No. US20030077601A1

GENERAL INFORMATION:

APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY

APPLICANT: HENDRICKSON, EDWIN

TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING

TITLE OF INVENTION: NUCLEIC ACID

TITLE OF INVENTION: SACTERIA

FILE REFERENCE: BC1002 US CIP

CURRENT FILING DATE: 2002-01-29

PRIOR PAPLICATION NUMBER: US 60/129,511

PRIOR PAPLICATION NUMBER: 60/129,511

PRIOR PLING DATE: 1999-04-15

PRIOR PILING DATE: 1999-04-15

SPIOR PILING DATE: 1999-04-15

NUMBER OF SEQ ID NOS: 103

SOFTWARE: Microsoft Office 97

SEQ ID NO 6

LINGTH: 1377
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Sequence 3, Application US/10061071

Sequence 3, Application US/10061071

Sequence 3, Application US/10061071

GENERAL INFORMATION:
APPLICANT: B.I. DUPONT DE NEMOURS & COMPANY
APPLICANT: HENDRATICNS:
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION: BACTERIA
FILE REFERENCE: BC1002 US CIP
CURRENT FILING DATE: 2002-01-29
FRIOR PILING DATE: 1999-04-15
FRIOR PLILING DATE: 1999-04-15
FRIOR PLILING DATE: 1999-04-15
FRIOR FILING DATE: 1999-04-15
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; OGGANISM: Dehalococcoides ethenogenes strain V/SFD
(S-10-061-071-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22; DB 15;
Pred. No. 0.00045;
; Mismatches 0;
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                        ; TYPE: DNA; ORGANISM: Dehalococcoides ethenogenes strain PIN US-10-061-071-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Dehalococcoides ethenogenes strain DLL
US-10-061-071-6
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Best Local Similarity 100.0%;
Matches 22; Conservative 0
                  SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGIH: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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OTHER INFORMATION: n=a or c or g or

FEATURE:
NAME/KEY: misc feature
LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c or g or t FEATURE:
NAME/KEY: misc\_feature
LOCATION: (12001)..(135000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (90001)..(105000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (135001)..(150000) JTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (150001)..(165000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (28501)..(300000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature OCATION: (240001)..(255000) THER INFORMATION: n=a or c or g or t FEATURE:
NAME/KEY: misc\_feature
LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (45001)..(60000) OTHER INFORMATION: n=a or c or g or LOCATION: (30001)..(45000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (105001)..(120000) OTHER INFORMATION: n=a or c or g or AME/KEY: misc feature LOCATION: (195701)..(210000) THER INFORMATION: n=a or c or g or NAME/KEY: misc\_feature LOCATION: (165001)..(180000) OTHER INFORMATION: n=a or c or g or WAME/KEY: misc feature OCATION: (180001)..(195000) DTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (210001)..(225000) THER INFORMATION: n=a or c or g or FEATURE:
NAME/FER: misc feature
NACATION: (255001)..(270000)
OTHER INFORMATION: n=a or c or g FEATURE: NAME/KEY: misc\_feature LOCATION: (225001)..(240000) OTHER INFORMATION: n=a or c or

NAME/KEY: misc feature LOCATION: (270001)..(285000) OTHER INFORMATION: n=a or c

FEATURE: NAME/KEY: misc\_feature LOCATION: (300001)..(315000)

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Publication No. US20020192672A1

GENERAL INFORMATION:
APPLICANT: Dawson, Jacqueline E.
APPLICANT: Anderson, Burt

TITLE OF INVENTION: Identification of a New Ehrlichia
TITLE OF INVENTION: Species from a Patient Suffering From Ehrlichiosis
TITLE OF INVENTION: Species from a Patient Suffering From Ehrlichiosis
CURRENT APPLICATION NUMBER: US/10/053,078

CURRENT FILING DATE: 2002-01-17

PRIOR APPLICATION NUMBER: U.S. 09/061770

PRIOR APPLICATION NUMBER: U.S. 07/687,526

PRIOR FILING DATE: 1991-04-18

PRIOR PILING DATE: 1991-04-18

PRIOR PILING DATE: U.S. 08/147,891
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APPLICANT: Doxsey, Stephen J.
TITLE OF INVENTION: NEW STRAINS OF MYCOPLASMA HYORHINIS AS
TITLE OF INVENTION: CAUSATIVE AGENT FOR SYSTEMIC SCLEROSIS
FILE REFERENCE: 07917-142001
CURRENT APPLICATION NUMBER: US/10/391,249
CURRENT PILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US 60/364,801
PRIOR APPLICATION NUMBER: US 60/364,801
PRIOR FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16; DB 17; Length 354; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Doxeey, Stephen J.
TITLE OF INVENTION: NEW STRAINS OF MYCOPLASMA HYORHINIS AS
TITLE OF INVENTION: CAUSATIVE AGENT FOR SYSTEMIC SCLEROSIS
FILE REPERENCE: 07917-142001
CURRENT APPLICATION NUMBER: US/10/391,249
CURRENT APPLICATION NUMBER: US/0/364,801
PRIOR APPLICATION NUMBER: US 60/364,801
PRIOR PILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 354
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100.0%; Pred. No. ...
0; Mismatches
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100.0%; Pre
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Best Local Similarity 100.0
Matches 16; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Mus musculus
US-10-391-249-17
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CORGANISM: Sus scrofa
US-10-391-249-18
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US-10-053-078-1/c
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US-10-391-249-16/C
| US-10-391-249-16/C
| Sequence 16, Application US/10391249
| Publication No. US20040091935A1
| GAPERAL INPORMATION:
| APPLICANT: Doxsey, Stephen J.
| TITLE OF INVENTION: NEW STRAINS OF MYCOPLASMA HYORHINIS AS |
| TITLE OF INVENTION: CAUGATIVE AGENT FOR SYSTEMIC SCLEROSIS |
| FILE REFERENCE: 07917-142001 |
| CURRENT FILING DATE: 2003-03-17 |
| PRIOR APPLICATION NUMBER: US 60/364,801 |
| PRIOR APPLICATION NUMBER: US 60/364,801 |
| PRIOR APPLICATION NUMBER: US 60/364,801 |
| PRIOR SEQ ID NOS: 43 |
| SOFTWARE FASESED for Windows Version 4.0 |
| SEQ ID NO 16 |
| LENGTH: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.7%; Score 16; DB 17; Length 244; 100.0%; Pred. No. 2.8; O; Mismatches 0; Indels
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Pred. No. 0.00033;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (67501)..(690000)
OTHER INFORMATION: n=a or c or g or
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              NAME/KEY: misc feature
LOCATION: (585001)...(600000)
OTHER INFORMATION: n=a or c or g
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                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or
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NAME/KEX: misc feature
LOCATION: (64501)..(660000)
OTHER INFORMATION: n=a or c or
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Best Local Similarity 100.0%;
Matches 22, Conservative 0
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                                                                                                          NAME/KEY: misc feature
LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c
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LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
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US-10-391-249-17/c
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TYPE: DNA

8 g

Search completed: August 4, 2004, 11:56:26 Job time : 201.06 secs

579 CCCGAGAACGTATTCA 564

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August 4, 2004, 04:00:30; Search time 180.771 Seconds (without alignments) 517.009 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                  3373863 segs, 2124099041 residues
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22
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Post-processing: Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

n	Description	Aad37948 16S ribos	Aad58507 16S ribos	Aad58049 Dehalococ	Aah28398 Intergeni	Aah28396 Intergeni	Aah28401 Intergeni	_	Aah28399 Intergeni	Aac62240 A 16S rDN	σ.	_		Aad57960 Dehalococ	Aad57958 Dehalococ	Aac62244 A 16S rDN	Aad57962 Dehalococ	Aaf31090 Bacterial	Aaf31089 Bacterial	Abs71617 Rickettsi	Abs71618 Borrelia		1 TT 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
SOUTH THE STATE OF	QI	AAD37948	AAD58507	AAD58049	AAH28398	AAH28396	AAH28401	AAH28397	AAH28399	AAC62240	AAD57959	AAD57957	AAD57961	AAD57960	AAD57958	AAC62244	AAD57962	AAF31090	AAF31089	ABS71617	ABS71618	AAX20248 04	
	DB	9	σ	œ	4	4	4	4	4	4	œ	œ	00	α	œ	4	ω	4	4	9	Y	N	
	Query Match Length	336	336	1014	1284	1284	1284	1284	1284	1335	1377	1377	1377	1377	1378	1443	1443	1451	1451	1479	1515	110000	
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Aaq36494 Mycoplasm	Aaq36491 Mycoplasm	Aaq36493 Mycoplasm						_	Aav43697 Ehrlichia	ы Ш	_	Acd26696 Ehrlichia	Acd26697 Ehrlichia	Abx93090 DNA seque	DNA	Aax61135 P36 ribos	_	Aad58050 Dehalococ	Abz79794 Mycoplasm	Abz79792 Mycoplasm	Abz79793 Mycoplasm	
AAQ36494	AAQ36491	AAQ36493	AAQ36490	AAQ36495	AAQ21032	AAQ21035	AAQ21034	AAQ15188	AAV43697	ADA18591	ADA18587	ACD26696	ACD26697	ABX93090	ABX93091	AAX61135	AAX61134	AAD58050	ABZ79794	ABZ79792	ABZ79793	
Ŋ	N	N	N	~	7	N	7	7	~	ω	œ	œ	ω	Φ	α	7	N	œ	7	7	7	
180	187	188	189	191	400	444	539	683	683	683	683	683	683	683	683	938	938	1385	1438	1445	1445	
2.7	2.7	2.7	72.7	72.7	2.7	72.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	72.7	7.7	2.7	
7	72	7	7	7	-	7	7	-	7	2	7	7	7	7	7	7	7	7	7	7	7	
16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	
c 24	c 25	c 26	c 27	c 58	c 29	30	c 31	32	33	34	35	c 36	C 37	38	33	C 40	c 41	24	C 43	C 44	C 45	

# ALIGNMENTS

RESULT 1

Bioremediative microorganism; 16S ribosomal subunit; dechlorination; PCB; polychlorinated biphenyl; biodegradation; halogenated organic waste; contaminated soil; leachate; aqueous surfactant solution; ds. Bioremediative microorganism for dechlorinating chlorinated biphenyls and for bioremediation, comprises a specific 168 ribosomal subunit nucleic (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST. AAD37948/c ID AAD37948 standard; DNA; 336 BP. 18-MAY-2001; 2001WO-US016030. 19-MAY-2000; 2000US-0205818P. 06-FEB-2001; 2001US-0266650P. 16S ribosomal DNA (rDNA) #2. 10-SEP-2002 (first entry) WPI; 2002-114266/15. May HD; WO200189729-A2. Unidentified 29-NOV-2001. Sowers KR, AAD37948; 

for bioremedia acid sequence.

Claim 1; Fig 22; 102pp; English.

The present invention relates to bioremediative microorganisms comprising 16S ribosomal subunit nucleic acid sequence. The microorganisms of the invention are useful for dechlorinating polychlorinated biphenyls (PCBs) including anaerobic dechlorination of ottho- and double-flanked chloro substituents of PCBs. They are useful for biodegradation of halogenated corganic waste, e.g., contaminated soil from landfill sites and river beds containing PCBs and to treat leachasts and aqueous surfactant solutions resulting from washing the organic waste to transfer PCBs to the aqueous surfactant solutions. The method of the invention is useful for

Dehalococcoides related family A 16S DHFA sequence. 16S rDNA, dechlorinating bacterial organism; ds.

20-NOV-2003

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determining the bioremediative potential of CB-containing site, which is useful for monitoring CB-containing site. The invention also relates to compositions which are useful for bioremediation. The present sequence is a 16S ribosomal DNA (rDNA) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to compositions and methods for bioremediation of polychlorinated biphenyls (PCBs) using dechlorinating microorganisms grown in the presence of stimulating halogenated hydrocarbons and polyhalogenated ethenes. Polyhalogenated ethenes are used to stimulate the growth and dechlorinating activity of PCB dechlorinating bacteria in a contaminated soil or sediment. The present
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stimulation of polychlorinated biphenyl dechlorinating bacteria contacting polychlorinated biphenyl dechlorinating bacteria with stimulant having polyhalogenated ethene(s).
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                                                                                                                                                                                                                                                                                                                 Polychlorinated biphenyls; PCBs; dechlorinating activity; ds.
                                                                                 100.0%; Score 22; DB 6; Length 336; 100.0%; Pred. No. 0.00072; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 22; DB 9; Length 336; 100.0%; Pred. No. 0.00072; ive 0; Mismatches 0; Indels
                                                            Sequence 336 BP; 76 A; 83 C; 97 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 336 BP; 76 A; 83 C; 97 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is 16S ribosomal subunit DNA
                                                                                                                                               323 ACAAGGCCCGAGAACGIAITCA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 4; 41pp; English
                                                                                                                                                                                                                                                                                          16S ribosomal subunit DNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                              03-FEB-2003; 2003WO-US003202
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2002; 2002US-0353134P
                                                                                                                                                                                                       AAD58507/c
ID AAD58507 standard; DNA; 336
                                                                                                                                                                                                                                                                  (first entry)
                                                                                Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                 WO2003065011-A2.
                                                                                                                                                                                                                                                                                                                                       Unidentified
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Novel isolated 16S rDNA sequence useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in

(DUPO ) DU PONT DE NEMOURS & CO E I.

Ebersole R, Hendrickson E;

WPI; 2003-636804/60.

30-JAN-2002; 2002WO-US003927. 30-JAN-2002; 2002WO-US003927.

WO2003064695-A1.

07-AUG-2003

Unidentified.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Intergenic spacer; Chlamydiaceae; 168 rRNA; 238 rRNA; Region A; Region B; chlamydial infection; ss.
                                                                                        The invention relates to an isolated 16S rDNA sequence indicative of a dechlorinating bacterial organism. The invention is useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in various samples. The method of the invention is useful for identifying a dechlorinating bacterial organism that is a member of a cell population or consortium. The isolated bacterial organism is useful for dechlorinating chlorinated compounds which
                                                                                                                                                                                                                                                         involves contacting a chlorinated compound with the organism. Oligomuclectide polymer of the invention is useful for separating subfamilies of dechlorinating bacterial organism. The present sequence is Dehalococcoides related family A 165 DHFA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Intergenic spacer between 168 and 23S rRNA genes of strain FML-12.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                             ch 100.0%; Score 22; DB 8; Length 1014; Similarity 100.0%; Pred. No. 0.0007; 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1014 BP; 256 A; 238 C; 309 G; 211 T; 0 U; 0 Other;
                                               Claim 1; Page 99-100; 110pp; English.
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1. .537
/*tag= b
/note= "Region A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1004 ACAAGGCCCGAGAACGTATTCA 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH28398/c
ID AAH28398 standard; rRNA; 1284 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydophila pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 22; Conserv
various samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-2003
17-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH28398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_RNA
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AAD58049 standard; DNA; 1014 BP

RESULT 3 AD58049/c ID AAD5804 XX

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Chlamydophila pneumoniae.
 chlamydial infection; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from Chlamydiaceae. The sequences comprise the intergenic spacer between the 16S and the 23S rRNA genes, including the far downstream end of the 16S and the far upstream end of the 23S and the far upstream end of the 23S and the far upstream end of the 23S and of Domain I (referred to as Region A), and secondarily, a 131 bp region in the 3' end of Domain I (referred to as Region B). The sequences provide suitable target sequences for developing probes and primers which are probes can be used to identify the presence of Chlamydiaceae. The primers and probes can be used to identify the presence of Chlamydiaceae in a test sample, or to distinguish one strain from another, and for diagnosing chlamydial infections in humans and animals. (Updated on 11-SBP-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intergenic spacer; Chlamydiaceae; 16S rRNA; 23S rRNA; Region A; Region B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH28371-AAH28413 represent intergenic spacer target sequences, derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Intergenic spacer between 16S and 23S rRNA genes of strain CWL-029.
                                                                                                                                                                                                                                                                                                                                                                                                                              New primers and probes derived from sequences of intergenic spacer between 16S and 23S genes and region of Domain I in 23S region of Chlamydiaceae, useful for assaying and identifying all strains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1284 BP; 394 A; 216 C; 330 G; 344 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 4; Lu
Pred. No. 0.00069;
; Mismatches 0;
                                                                                                                                                         23S rRNA
                                                             /*tag= c
/note= "intergenic spacer"
445. .1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Col 119-120; 89pp; English.
                                                                                                                                             /*tag= d
'note= "Domain I of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAAGGCCCGAGAACGTATTCA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                                 /*tag= e
/note= "23S rRNA"
445. .1063
                                                                                                                                                                                               'note= "Region B"
    1. .221
/*tag= a
/note= "168 rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396/c
AAH28396 standard; rRNA; 1284 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                   98US-00052333
                                                                                                                                                                                                                                                                                      98US-00052333
                                                                                                                                                                     959. .1086
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                           Everett KDE, Andersen AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                             222. .444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                              OF AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-440857/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                              (USDA ) US SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydiaceae.
                                                                                                                                                                                                                                                                                      31-MAR-1998;
                                                                                                                                                                                                                                                                                                                   31-MAR-1998;
                                                                                                                                                                                                                                US6261769-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-2003
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                                                                                                                                                                                                                                                           17-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH28396;
                                             misc_RNA
                                                                                                                                                                          misc RNA
                                                                                                                                rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH28396/AAH2
XX
XX
AC AAH2
XX
DT 11-S
DT 17-S
XX
DE Inte
XX
XW Inte
    rRNA
                                                                                       rRNA
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from Chlamydiaceae. The sequences comparise the intergenic spacer between the 16S and the 23S rRNA genes, including the far downstream end of the 16S and the far upstream end of the 23S domain I flanking intergenic spacer (referred to as Region A), and secondarily, a 131 bp region in the 3' end of Domain I (referred to as Region B). The sequences provide suitable target sequences for developing probes and primers which are useful for identifying and detecting chlamydiaceae. The primers and probes can be used to identify the presence of Chlamydiaceae in a test sample, or to distinguish one strain from another, and for disanosing chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to strandardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH28371-AAH28413 represent intergenic spacer target sequences, derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New primers and probes derived from sequences of intergenic spacer between 16S and 23S genes and region of Domain I in 23S region of Chlamydiaceae, useful for assaying and identifying all strains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1284 BP; 394 A; 218 C; 329 G; 343 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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/note= "Domain I of 23S rRNA"
959. .1086
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                                                                                                                                                                                         '*tag= c
'note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 113-116; 89pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
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                      (*tag= b
/note= "Region A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH28401 standard; rRNA; 1284 BP.
                                                                                                               /*tag= a
/note= "168 rRNA"
                                                                                                                                                                                                                                                              /*tag= e
/note= "23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Region B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACAAGGCCCGAGAACGTATTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-00052333
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                                                                                                                                                                                                                              .1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Everett KDE, Andersen AA;
                                                                                                                                                                                                                                                                                                      .1063
                                                                                                                                                              .444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USDA ) US SEC OF AGRIC.
                                                                                                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                   445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-440857/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydiaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6261769-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                           misc RNA
                                                                                                                                                                misc_RNA
                                                                                                                                                                                                                                                                                                                                                                           misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH28401/c
ID AAH284(
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                   rRNA
                                                                                                                                                                                                                                                                                                        rrna
                                                                                                rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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(revised)
(first entry)
                                                                                                   Chlamydiaceae.
                                                                                     Everett KDE,
                                                                US6261769-B1
                                                                        31-MAR-1998;
                                                                             31-MAR-1998;
   11-SEP-2003
17-SEP-2001
                                                                    17-JUL-2001,
                          misc_RNA
                                      misc_RNA
                                                        misc_RNA
                                            rRNA
                                rRNA
                                                  rRNA
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AAH28371-AAH28413 represent intergenic spacer target sequences, derived from Chlamydiaceae. The sequences comprise the intergenic spacer between the 16S and the 23s rNAM genes, including the far downstream end of the 16S and the far upstream end of the 23S domain I flanking intergenic spacer (referred to as Region A), and secondarily, a 131 bp region in the 3' end of Domain I (referred to as Region B). The sequences provide suitable target sequences for developing probes and primers which are useful for identifying and detecting Chlamydiaceae. The primers and probes can be used to identify the presence of Chlamydiaceae in a test sample, or to distinguish one strain from another, and for diagnosing chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
                                                                    Intergenic spacer, Chlamydiaceae; 16S rRNA; 23S rRNA; Region A; Region B; chlamydial infection; ss.
Intergenic spacer between 16S and 23S rRNA genes of strain TW-183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New primers and probes derived from sequences of intergenic spacer between 16S and 23S genes and region of Domain I in 23S region of Chlamydiaceae, useful for assaying and identifying all strains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1284 BP; 394 A; 216 C; 330 G; 344 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= d
/note= "Domain I of 23S rRNA"
959. .1086
/note= "Region B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 125-128; 89pp; English.
                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  1. .221
/*tag= a
/note= "16S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= e
/note= "23S rRNA"
145. .1063
                                                                                                                                                                                                                                                                                                                                         note= "Region A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1284
                                                                                                                                                                                                                                                                            1. .537
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersen AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444
                                                                                                                                                                    Chlamydophila pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USDA ) US SEC OF AGRIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-440857/47.
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AAH28171-AAH28413 represent intergenic spacer target sequences, derived from Chlamydiaceae. The sequences comprise the intergenic spacer between the 16S and the 23S rRNA genes, including the far downstream end of the 16S and the far upstream end of the 23S domain I flanking intergenic spacer (referred to as Region A), and secondarily, a 131 bp region in the 3' end of Domain I (referred to as Region B). The sequences provide suitable target sequences for developing probes and primers which are useful for identifying and detecting Chlamydiaceae. The primers and probes can be used to identify the presence of Chlamydiaceae in a test sample, or to distinguish one strain from another, and for diagnosing chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                     Intergenic spacer, Chlamydiaceae, 16S rRNA; 23S rRNA; Region A; Region B; chlamydial infection; ss.
                                                                                                                                                                           Intergenic spacer between 16S and 23S rRNA genes of strain CWL-1011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New primers and probes derived from sequences of intergenic spacer between 16S and 23S genes and region of Domain I in 23S region of Chlamydiaceae, useful for assaying and identifying all strains of Chlamydiaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                  *tag= c
note= "intergenic spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Col 115-118; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= d
note= "Domain I of
                                                                                                                                                                                                                                                                       Location/Qualifiers
67 ACAAGGCCCGAGAACGTATTCA 46
                                                                                                                                                                                                                                                                                                /*tag= b
/note= "Region A"
                                                                                                                                                                                                                                                                                                                                        '*tag= a
'note= "16S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Region B"
                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= e
'note= "23S rRNA"
                                                                                 AAH28397 standard; rRNA; 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00052333.
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/*tag= f
                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         45. .1284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersen AA;
                                                                                                                                                                                                                                                                                                                                                                    .444
                                                                                                                                                                                                                                           Chlamydophila pneumoniae.
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                                                                                                                                     (revised)
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                                                                                                                                     11-SEP-2003
17-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6261769-B1
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                                                                                                           AAH28397;
                                                                                                                                                                                                                                                                                  misc_RNA
                                                                                                                                                                                                                                                                                                                                                                  misc_RNA
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                                                                   AAH28397/c
                                                                                                                                                                                                                                                                                                                            rRNA
                                                                                                                                                                                                                                                                                                                                                                                                          rRNA
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                                                      RESULT 7
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Gaps

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0; Indels

0; Mismatches

100.0%; Score 22; DB 4; Length 1284; 100.0%; Pred. No. 0.00059;

. Matches

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and secondarily, a 131 bp region in the
                                                                                                                                 22
                                                                                                                                              67 ACAAGGCCCGAGAACGTATTCA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACAAGGCCCGAGAACGTATTCA 22
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                                                                                                                                  1 ACAAGGCCCGAGAACGTATTCA
                                                                                                                                                                                              AAC62240 standard; DNA; 1335 BP
                                                                                                                 .
0
                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                  Ebersole RC;
                                                                                                                                                                                                                                                                                                                                                             13-APR-2000; 2000WO-US009883
                                                                                                                                                                                                                                                                                                         Dehalococcoides ethenogenes
                                                                                                                                                                                                                                  19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-024581/03.
                                                                                                       Local Similarity
es 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                  Hendrickson ER,
                                                             standardise OS
                                                                                                                                                                                                                                                                                                                          WO200063443-A2
                                                                                                                                                                                                                                                                                                                                                                              15-APR-1999;
                                                                                                                                                                                                                                                                                                                                            26-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                               Query Match
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Matches
                                                                                                                 Matches
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                                                                                                                                                                                                          spacer; Chlamydiaceae; 16S rRNA; 23S rRNA; Region A; Region B;
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from Chlamydiaceae. The sequences comprise the intergenic spacer between
the 16S and the 23S rRNA genes, including the far downstream end of the
16S and the far upstream end of the 23S domain I flanking intergenic
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New primers and probes derived from sequences of intergenic spacer between 16S and 23S genes and region of Domain I in 23S region of Chlamydiaceae, useful for assaying and identifying all strains of
                                                                                                                                                                                        Intergenic spacer between 168 and 238 rRNA genes of strain FML-16.
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0
                           Length 1284;
          Sequence 1284 BP; 392 A; 218 C; 331 G; 343 T; 0 U; 0 Other;
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                           DB 4; I
0.00069;
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note= "Domain I of 23S rRNA"
                                             Mismatches
                                                                                                                                                                                                                                                                                                                                   note= "intergenic spacer"
                           Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 121-122; 89pp; English.
                                                                                                                                                                                                                                                     location/Qualifiers
                                                                           ACAAGGCCGAAACGTATTCA 46
                                                              1 ACAAGGCCCGAGAACGTATTCA 22
                                                                                                                                                                                                                                                                                                                                                                                                  959. .1086
/*tag= f
/note= "Region B"
                                                                                                                                                                                                                                                                                       |. .221
|*tag= a
|note= "16S rRNA"
                                                                                                                                                                                                                                                                                                                                                     *tag= e
'note= "23S rRNA"
                                                                                                                                                                                                                                                                               note= "Region A"
                                                                                                                 AAH28399/c
ID AAH28399 standard; rRNA; 1284 BP
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                          100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                 222. .444
/*tag= c
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                                                                                                                                                                                                                                                               ...537
*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andersen AA;
                                                                                                                                                                                                                                   Chlamydophila pneumoniae.
                                                                                                                                                                                                                   infection; ss
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                                                                                                                                                              (revised)
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                        Query Match
Best Local Similarity
Matches 22; Conser
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                                                                                                                                                             11-SEP-2003
17-SEP-2001
                                                                                                                                                                                                          Intergenic
chlamydial
                                                                                                                                                                                                                                                      Key
misc_RNA
                                                                                                                                            AAH28399
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                                                                                                                                                                                                                                                                                                                                                                                                  misc RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       etherogenes strain STF, isolated from soil surrounding an industrial site. The 16S rDNA profile is linked to dechlorinating activity. Bacterial strain comprising the 16S rDNA sequence of the invention are useful for the dechlorination of chlorinated compounds such as carbontetrachloride, tetrachloroethane, chloride, and chloromethane, trichhoroethane, dichloroethylene, viryl chloride, and chloroaromatics. The 16S rDNA sequence is also useful for identification of new chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the 16S rDNA profile of Dehalococcoides
spacer (referred to as Region.A), and secondarily, a 131 bp region in t 3 end of Domain I (referred to as Region B). The sequences provide suitable target sequences for developing probes and primers which are useful for identifying and detecting Chlamydiaceae. The primers and probes can be used to identify the presence of Chlamydiaceae in a test sample, or to distinguish one strain from another, and for diagnosing chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1284;
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                                                                                                                                                                                                                                                                                                                                                           Seguence 1284 BP; 394 A; 216 C; 330 G; 344 T; 0 U; 0 Other;
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100.0%; Pred. No. 0.00069;
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Dehalococcoides ethenogenes.
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                                                                                                                                                                                                                                                                                                                                      Novel isolated 16S rDNA sequence useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in
                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated 16S rDNA sequence indicative of a dechlorinating bacterial organism. The invention is useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in various samples. The method of the invention is useful for identifying a dechlorinating bacterial organism that is a member of a cell population or consortium. The isolated bacterial organism that is involves contacting a chlorinating chlorinated compounds which involves contacting a chlorinated compound with the organism. Oligonucleotide polymer of the invention is useful for separating subfamilies of dechlorinating bacterial organism. The present sequence is
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                                                                                                                         Dehalococcoides ethenogenes strain DAB 16S rDNA (DHE-DAB).
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                                                                                                                                             16S rDNA; dechlorinating bacterial organism; ds
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        1322 ACAAGGCCCGAGAACGTATTCA 1301
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                                                    959/c
AAD57959 standard, DNA, 1377 BP.
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                                                                                                                                                                   Dehalococcoides ethenogenes
                                                                                                                                                                                                                                                                                              Ebersole R, Hendrickson E;
                                                                                                     (first entry)
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Best Local Similarity
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                                                                                AAD57959;
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                                      RESULT 10
AAD57959/c
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The invention relates to an isolated 16S rDNA sequence indicative of a dechlorinating bacterial organism. The invention is useful for forming probes and primers which are useful for identifying dechlorinating to useful for identifying dechlorinating useful for identifying a dechlorinating bacterial organism that is a member of a cell population or consortium. The isolated bacterial organism that is a involves contacting a chlorinating chlorinated compounds which involves contacting a chlorinated compound with the organism. Oligonuclectide polymer of the invention is useful for separating collinating chlorinating chlorinating subfamilites of dechlorinating bacterial organism. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated 16S rDNA sequence useful for forming probes and primers which are useful.for identifying dechlorinating bacterial organism in
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AAD57961/c
ID AAD57961 standard; DNA; 1377
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WO2003064695-A1
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Dehalococcoides ethenogenes 16S rDNA
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AAC62244/c
ID AAC62
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AAD57958/c
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                                                                                              dechlorinating bacterial organism. The invention is useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in various samples. The method of the invention is useful for identifying a dechlorinating bacterial organism that is a member of a cell population or consortium. The isolated bacterial organism is useful for dechlorinating chlorinated compounds which
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Oligomuclectide polymer of the invention is useful for separating subfamilies dechlorinating bacterial organism. The present sequence is behalococcoides ethenogenes 16S rDNA
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Novel isolated 16S rDNA sequence useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in various samples.
                                                                                     invention relates to an isolated 16S rDNA sequence indicative of a
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Pred. No. 0.00069;
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                                                          Claim 31; Fig 1; 110pp; English
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD57960;
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
AAD57960/c
                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated 16S rDNA sequence useful for forming probes and primers which are useful for identifying dechlorinating bacterial organism in
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                                                                                                           Gaps
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Pred. No. 0.00069;
Sequence 1377 BP; 357 A; 299 C; 415 G; 306 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1378 BP; 361 A; 300 C; 413 G; 304 T; 0 U; 0 Other;
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                                                 Score 22; DB 8; I
Pred. No. 0.00069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16S rDNA; dechlorinating bacterial organism;
                                                    100.0%; Score 22; DB
Similarity 100.0%; Pred. No. 0.0
22; Conservative 0; Mismatches
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                                                                                                                                                                1 ACAAGGCCCGAGAACGTATTCA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 31; Fig 1; 110pp; English
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AAD57958 standard; DNA; 1378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2002; 2002WO-US003927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dehalococcoides ethenogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ebersole R, Hendrickson E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2003 (first entry)
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Best Local Similarity 100.
Matches 22; Conservative
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                                                 Query Match
Best Local Simil
Matches 22;
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us-09-940-860-3.0ligo.rng

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The present sequence represents the 16S rDNA profile of Dehalococcoides ethenogenes strain 195. The 16S rDNA profile is linked to dechlorinating activity. Bacterial strain comprising the 16S rDNA sequence of the invention are useful for the dechlorination of chlorinated compounds such as carbontetrachloride, tetrachlorocthane, chloroform, dichloromethane, trichlorocethane, dichlorocethylene, vinyl chloride, and chloroacomatics. The 16S rDNA sequence is also useful for identification of new chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
                                                                                                                      16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride; carbontetrachloride; tetrachloroethane; chloroform; dichloromethane; trichloroethane; dichloroethylene; chlorinating bacteria; ss.
                                                                                     A 16S rDNA sequence indicative of a chlorinating bacterial strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New 16S rDNA profile derived from Dehalococcoides ethenogenes and indicative of a dechlorinating bacterial strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1443 BP; 379 A; 306 C; 443 G; 314 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 49-50; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                        Hendrickson ER, Ebersole RC;
                                                                                                                                                                                                                                                                                                             13-APR-2000; 2000WO-US009883.
                                                                                                                                                                                                                                                                                                                                                15-APR-1999; 99US-0129511P.
                                                                                                                                                                                                  Dehalococcoides ethenogenes
                                                  19-MAR-2001 (first entry)
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                                                                                                                                                                                                                                   WO200063443-A2.
               AAC62244;
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1329 ACAAGGCCCGAGAACGTATTCA 1308 1 ACAAGGCCCGAGAACGTATTCA 22 ઠે

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Gaps

; 0

Query Match 100.0%; Score 22; DB 4; Length 1443; Best Local Similarity 100.0%; Pred. No. 0.00069; Matches 22; Conservative 0; Mismatches 0; Indels

4, 2004, 06:43:37 Search completed: August Job time: 182.771 secs

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August 4, 2004, 06:43:54; Search time 208.988 Seconds (without alignments) 247.629 Million cell updates/sec
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1: /cgn2 6/ptodata/2/pna/PCT NEW COMB.seq:*
2: /cgn2 6/ptodata/2/pna/USOF NEW COMB.seq:*
3: /cgn2 6/ptodata/2/pna/USO7 NEW COMB.seq:*
5: /cgn2 6/ptodata/2/pna/USO8 NEW COMB.seq:*
5: /cgn2 6/ptodata/2/pna/USO8 NEW COMB.seq:*
6: /cgn2 6/ptodata/2/pna/USO9 NEW COMB.seq:*
7: /cgn2 6/ptodata/2/pna/USO1 NEW COMB.seq:*
8: /cgn2 6/ptodata/2/pna/USI0 NEW COMB.seq2:*
8: /cgn2 6/ptodata/2/pna/USI0 NEW COMB.seq3:*
9: /cgn2 6/ptodata/2/pna/USI0 NEW COMB.seq3:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              4754066 segs, 1232178907 residues
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                                                                                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                  1 gtgccagcagcagcggtaata 21
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		no				-	174, App		47421, A				-			347, App			139649,		٠.	146825,		11322, A	43,	43,
		Description	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence
SUMMARIES		ID	US-10-864-684-581	PCT-US03-41761-45189	PCT-US03-41761-45189	PCT-US03-41766A-45189	PCT-US03-36229-174	PCT-US04-17686-2493	US-10-425-115-47421	US-10-425-115-79433	US-10-669-143-12	US-10-835-208-10	PCT-US04-05092-48	US-10-767-471-10719	US-10-425-115-139088	PCT-US04-12047-347	US-10-425-115-49000	US-10-425-115-44757	US-10-425-115-139649	US-10-425-115-152690	US-10-425-115-171414	US-10-425-115-146825	US-10-425-115-146920	US-10-767-701-11322	PCT-US04-02974-43	US-10-770-668-43
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ď	Query	Match	81.0	81.0	81.0	81.0	76.2	76.2	76.2	76.2	76.2	76.2	76.2	76.2	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4
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Sequence 34028, A Sequence 34028, A Sequence 2411, App Sequence 111, App Sequence 179268, Sequence 179268, Sequence 29, Appl Sequence 29, Appl Sequence 145, App Sequence 163, App Sequence 563, App Sequence 663,			gth 1542; Indels 0; Gaps 0;	MS FOR INFERRING BOVINE BREED
1 PCT-US03-41761-34028 1 PCT-US03-41761-34028 1 PCT-US03-41766A-34028 1 PCT-US03-41766A-34028 6 US-10-425-115-10996 6 US-10-425-115-179268 7 US-10-796-174-56 1 US-10-796-174-56 1 US-10-796-174-56 1 US-10-796-174-56 1 US-10-791-179-179-179-179-179-179-179-179-179	ALIGNMENTS	3/10864684 120 121a 121a 121a 1210/864,684 106-08 3.1	; Score 17; DB 8; Len 8; Pred. No. 9.6; 0; Mismatches 0; 19	PC/TUS0341761 NC. 1 id ITIONS, METHODS, AND SYSTEMS: PCT/US03/41761 12-31 US 60/437,482
25 15 71.4 1126 28 15 71.4 1126 29 15 71.4 1126 29 15 71.4 1167 29 15 71.4 1167 31 15 71.4 1167 31 15 71.4 1163 32 15 71.4 1636 33 15 71.4 1751 35 15 71.4 1751 36 15 71.4 3884 37 10 15 71.4 3884 38 15 71.4 3884 39 15 71.4 3884 41 15 71.4 3884 42 15 71.4 3884 43 15 71.4 3884 44 15 71.4 5337 45 16 77.7		RESULT 1  US-10-864-684-581/c Sequence 581, Application US/1086468 GENERAL INFORMATION: APPLICANT: Scarlato, Vincenzo APPLICANT: Rappuoli, Rino APPLICANT: Rappuoli, Rino APPLICANT: Pizza, Mariagrazia APPLICANT: Grandi, Guido TITLE OF INVENTION: Neisserial Anti- FILE REFERENCE: CHIRO16 CURRENT APPLICATION NUMBER: US/10/8 CURRENT FILING DATE: 2004-06-08 NUMBER OP SEQ ID NOS: 1168 SOFTWARE: PatentIn version 3.1 LENGTH: 1542 TYPE: DNA ORGANISM: Neisseria gonorrhoeae US-10-864-684-581	Query Match Best Local Similarity 100.0% Matches 17; Conservative Qy 3 GCCAGCAGCAGCAGCAGTAA 1 Db 1148 GCCAGCAGCAGCAGTAA 1	PECSULT 2 PCT-45189/C PCT-45189, Application PC/TUS0341761 Sequence 45189, Application PC/TUS0341761 GENERAL INFORMATION: APPLICANT: MM GENOMICS, INC. APPLICANT: CHARTERIS, Paul APPLICANT: ROSENFELD, David APPLICANT: ROSENFELD, David APPLICANT: ROSENFELD, David APPLICANT: ROSENFELD, David APPLICANT: BATES, Stephen TITLE OF INVENTION: COMPOSITIONS, METHODE FILE REFERENCE: MMI1150WO CURRENT APPLICATION NUMBER: PCT/US03/417, CURRENT PILING DATE: 2003-12-31 PRIOR PILING DATE: 2002-12-31 NUMBER OF SEQ ID NOS: 64922
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PCT-US03-36229-174; Sequence 174, Application PC/TUS0336229; GENERAL INFORMATION:
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; Sequence 47421, Application US/10425115
; GENERAL INFORMATION:
                                                                                                                                                                    2268 GIGCCAGCAGCGGT 2252
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Best Local Similarity 100.0%; P.
Matches 16; Conservative 0;
                                                                                                                           1 GTGCCAGCAGCAGCGGT 17
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                                                 Local Similarity 100.
nes 17; Conservative
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ORGANISM: Mus musculus
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Sequence 45189, Application PC/TUSO341761

Sequence 45189, Application PC/TUSO341761

SEQUENCE 45189, Application PC/TUSO341761

APPLICANT: MAI GENOMICS, INC.

APPLICANT: DeNISE, Sue K.

APPLICANT: CHARTERIS, Paul

APPLICANT: HOLM, Tow

APPLICANT: HOLM, Tow

TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING BOVINE BREED

TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING BOVINE BREED

TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING BOVINE BREED

CURRENT APPLICATION NUMBER: PCT/USO3/41761

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR APPLICATION NUMBER: US 60/437,482

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MAI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: DENISE, Sue K.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS, METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REPERENCE: MMI1100WO
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                                                                                                                                                                       Score 17; DB 1; Length 2838; Pred. No. 9.7;
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                                                                                                                                                                    Query Match

81.0%; Score 17; DB

Best Local Similarity 100.0%; Pred. No. 9.7

Matches 17; Conservative 0; Mismatches
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; Sequence 45189, Application PC/TUS0341766A
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SEG ID NO 45189
LENGTH: 2838
                                                                      ; TYPE: DNA
; ORGANISM: Bovine 19866880933064
PCT-US03-41761-45189
                                                                                                                                                                                                                                                                                                                    2268 GIGCCAGCAGCAGCGGT 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Bovine 19866880933064
PCT-US03-41761-45189
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                                                                                                                                                                                                                                                                          1 GTGCCAGCAGCAGCGGT 17
SOFTWARE: PatentIN version 3.1
SEQ ID NO 45189
LENGTH: 2838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY APPLICANT: THE SCRETARY, DEPARTMENT OF THEALTH AND HUMAN SERVICES, CENTERS APPLICANT: FOR DISEASE CONTROL AND PREVENTION PRIMERS OF TILES OF INVENTION: PNI MICROARRAY AND USES
FILE REFERENCE: 14114.0375PI
CURRENT APPLICATION NUMBER: PCT/US04/17686
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: 60/475,915
PRIOR APPLICATION NUMBER: 60/475,915
PRIOR PLILNG DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 3085
SEC ID NO 2493
LENGTH: 783
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81.0%; Score 17; DB 1; Length 2838; 100.0%; Pred. No. 9.7; ive 0; Mismatches 0; Indels
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TITLE OF INVENTION: Nuclear Receptor-Based Diagnostic,
TITLE OF INVENTION: Therapeutic and Screening Methods
FILE REFERENCE: 50001/014W02
CURRENT APPLICATION NUMBER: PCT/US03/36229
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/426,305
PRIOR APPLICATION NUMBER: 60/426,305
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 198
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 174
LENGTH: 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match (76.2%; Score 16; DB 1; Best Local Similarity 100.0%; Pred. No. 31; Matches 16; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.2%; Score 16; DB 1;
100.0%; Pred. No. 31;
tive 0; Mismatches
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RESULT 10

US-10-835-208-10

US-10-835-208-10

Sequence 10, Application US/10835208

SEQUENCE 10, Application US/10835208

SEQUENCE 10, Application US/10835208

APPLICANT: Rosanne M. Crooke

APPLICANT: Rosanne M. Arraham

TITLE OF INVENTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION

FILE REFERENCE: ISPH-0593

CURRENT APPLICATION NUMBER: US/09/919,197

PRIOR APPLICATION NUMBER: US/09/919,197

PRIOR PILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 89

SOFTHARE FRANCE: ESEC for Windows Version 4.0

LENGTH: 1119
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                                                                            APPLICANT: Christopher J. Kirk
APPLICANT: Christopher J. Kirk
APPLICANT: Christopher J. Kirk
APPLICANT: Christopher J. Kirk
APPLICANT: Gin Zhang
APPLICANT: Agnes Choppin
TITLE OF INVENTION: Targeted Gene Disruptions, Compositions
TITLE OF INVENTION: Targeted Gene Disruptions, CURRENT APPLICANTON NUMBER: US/10/669,143
FILE REFERENCE: R-DB-13
PRIOR APPLICATION NUMBER: US 60/413,647
PRIOR APPLICATION NUMBER: US 60/413,666
PRIOR PILING DATE: 2002-09-24
PRIOR FILING DATE: 2002-09-24
PRIOR FILING DATE: 2002-09-24
PRIOR FILING DATE: 2002-09-24
PRIOR FILING DATE: 2002-09-24
PRIOR PELLOR NUMBER: US 60/413,655
PRIOR PELLOR NUMBER: US 60/413,655
PRIOR PELLOR NUMBER: US 60/413,625
PRIOR FILING DATE: 2002-09-24
PRIOR PRIOR PRIOR DATE: 2002-09-24
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Pred. No. 31;
0; Mismatches 0; Indels
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; Pred. No. 31; 
0; Mismatches 0; Indels
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76.2%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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100.0%;
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                                         Thomas J. Brennan
Catherine Guenther
Robert Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 16; Conservative
              Helen Baribault
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; CRGANISM: Mus musculus
US-10-669-143-12
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LOCATION: (33)...(815)
US-10-835-208-10
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 47421
LENGTH: 815
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US-10-25-115-79433/C
Sequence 79433, Application US/10425115
Sequence 79433, Application US/10425,115
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; OTHER INFORMATION: Clone ID: MRT4577_143255C.1
US-10-425-115-47421
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                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (1)..(815)
OTHER INFORMATION: unsure at all n locations
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GENERAL INFORMATION:
APPLICANT: William Matthews
APPLICANT: Mark Moore
APPLICANT: Russell Phillips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mark Moore
Russell Phillips
Michael V. Wiles
Thadd C. Reeder
Robert G. Wisotzkey
Keith D. Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 GCCAGCAGCAGCGGTA 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100."
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Zea mays
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US-10-669-143-12
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APPLICANT:
APPLICANT:
APPLICANT:
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Query Match
Best Local Similarity 100.
Matches 15, Conservative
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ORGANISM: Zea mays
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GENERAL INFORMATION
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS, METHODS OF DETECTION AND USES THEREOF
FILE REPERBENCE: CLOOISOS
CURRENT APPLICATION NUMBER: 1204-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 10719
LINGTH: 109725
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                                           GENERAL INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: MARGUIS, Joseph P.; SWARNAKAR, Anita,
APPLICANT: CHAWLA, Narinder K.;
APPLICANT: CHAWLA, Narinder K.;
APPLICANT: CHAWLA, Narinder K.;
APPLICANT: HAFALIA, April J.A.; RICHARDSON, Thomas;
APPLICANT: HAFALIA, April J.A.; RICHARDSON, Thomas;
APPLICANT: GACKSON, Alan; YANG, Junning;
APPLICANT: DATE: 2004-02-20
CURRENT FILING DATE: 2003-02-0
PRIOR APPLICATION NUMBER: US 60/449,059
PRIOR APPLICATION NUMBER: US 60/449,059
PRIOR APPLICATION NUMBER: US 60/456,932
PRIOR APPLICATION NUMBER: US 60/466,678
PRIOR PILING DATE: 2003-03-19
PRIOR FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PERL PROGRAM
SEQ ID NOS: 92
SEQ ID NOS: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7523794CB1
PCT-USO4-05092-48
Application PC/TUS0405092
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Best Local Similarity 100.
Matches 16; Conservative
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ORGANISM: Homo sapiens
US-10-767-471-10719
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 16; Conserva
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26803 AGCAGCAGCGGTAATA 26788

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APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: About K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: 18-21 (35222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 139088
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100.0%; Pred. No. 97;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: MRT4577_58330C.1
US-10-425-115-139088
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PRIOR APPLICATION NUMBER: US 60/463,732
PRIOR FILING DATE: 2003-04-18
PRIOR PLILNG DATE: 2003-04-18
PRIOR APPLICATION NUMBER: US 60/467,230
PRIOR APPLICATION NUMBER: US 60/467,130
PRIOR PILING DATE: 2003-05-02
PRIOR PELLING DATE: 2003-05-02
PRIOR PILING DATE: 2003-05-02
PRIOR PELLING DATE: 2003-06-08
PRIOR PILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: US 60/493,573
PRIOR PILING DATE: 2003-09-08
PRIOR PILING DATE: 2003-00-03
PRIOR PILING DATE: 2003-00-03
PRIOR PILING DATE: 2003-07-03
PRIOR PILING DATE: 2003-07-03
PRIOR PILING DATE: 2003-07-03
PRIOR PILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: US 60/471,306
PRIOR PILING DATE: 2003-07-03
PRIOR PILING DATE: 2003-05-19
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Sequence 139088, Application US/10425115 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CT-US04-12047-347/c
Sequence 347, Application PC/TUS0412047
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 GTGCCAGCAGCAGCG 124
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ORGANISM: Homo sapiens
PCT-US04-12047-347
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Best Local Similarity
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WS-10-425-115-49000/c

Sequence 49000, Application US/10425115

Sequence 49000, Application US/10425115

Sequence 49000, Application US/10425115

Sequence 49000, Application US/10425115

APPLICANT: La Rosa, Thomas J.

APPLICANT: Avair, David K.

APPLICANT: Cao, Yinua

APPLICANT: Cao, Youguei

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 49000

LENGTH: 260
  Gaps
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0; Indels
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CRCANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_144694C.1

US-10-425-115-49000
0; Mismatches
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15; Conservative
Matches
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Search completed: August 4, 2004, 11:43:47 Job time : 209.988 secs

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Sequence:

Run on:

Searched:

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385.436 Million cell updates/sec
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15: /cgn2 6/ptodata/2/pna/US087 COMB.seq:*
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/cgn2_6/ptodata/2/pna/US100A_COMB.seq:
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                 - nucleic search, using sw model
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Perfect score:
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6/ptodata/2/pna/US10B_COMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Gaps

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Length 21; Indels

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Query Match
100.0%; Score 21; DB 39;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 21; Conservative 0; Mismatches 0;
; OTHER INFORMATION: SYNTHETIC amplification primer US-09-940-860-4
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                                                                                 US-09-940-860-4
US-09-369-922-1
US-00-369-922-1
US-60-128-439-3619
US-60-128-439-4848
US-60-128-439-4848
US-60-128-439-3158
US-60-128-439-3158
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US-60-128-439-2469
US-60-128-439-2469
US-60-128-439-849
US-60-128-439-849
US-60-128-439-3517
US-60-128-439-3517
US-60-128-439-3517
US-60-128-439-3517
US-60-128-439-3518
US-60-128-439-4950
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US-00-128-439-1486
US-00-540-235-485
US-09-540-235-3580
US-00-540-235-4659
US-00-540-235-2070
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US-60-128-439-4162
US-09-540-235-453
US-60-128-439-679
US-60-128-439-913
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-60-128-439-1726
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-60-128-439-4897
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                         Query
Match Length DB
                                                                                 Score
                         Result
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## ALIGNMENTS

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Sequence 4, Application US/09940860

GENERAL INFORMATION:
APPLICANT: Rothman. Richard;
APPLICANT: Maulik
TITLE OF INVENTION: MOLECTLAR DIAGNOSIS OF BACTEREMIA
FILE REFERENCE: 01107.0018 S
CURRENT APPLICATION NUMBER: US/09/940,860
CURRENT FILING DATE: 2001-08-29
FRIOR PAPLICATION NUMBER: 60/229,376
FRIOR APPLICATION NUMBER: 60/229,376
FRIOR APPLICATION NUMBER: 60/229,376
SPRIOR APPLICATION NUMBER: 60/229,376
SPRIOR PRIOR PRIOR SEQ ID NOS: 7
SEQ ID
RESULT 1
US-09-940-860-4
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TYPE: DNA ORGANISM: Artificial Sequence FEATURE:

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RESULT 2
US-09-369-922-1
Sequence 1. Application US/09369922
GENERAL INFORMATION:
APPLICANT: Ting Robert C.
APPLICANT: Ting Robert C.
APPLICANT: Than, Jill M.
APPLICANT: Than, Jill M.
APPLICANT: Theres M.
ITILE OF INVENTION: Diagnosis of Plasmodium Infection by Analysis of TITLE OF INVENTION: Extrachromosomal Genetic Material
ITILE OF INVENTION: Diagnosis of Plasmodium Infection by Analysis of TITLE OF INVENTION: Extrachromosomal Genetic Material
ITILE OF INVENTION: Diagnosis of Plasmodium Infection by Analysis of TITLE OF INVENTION: Diagnosis of Plasmodium Infection by Analysis of TITLE REFERENCE: 64-99
CURRENT APPLICATION NUMBER: PCT/IB98/00212
PRIOR FILING DATE: 1997-08-06
PRIOR FILING DATE: 1997-09-16
PRIOR FILING DATE: 1997-04-21
PRIOR FILING DATE: 1997-02-06
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PARENTH FALOR
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JOS-09-1992C.

GENERAL INFORMATION:

APPLICANT: ATA, Anna K.

APPLICANT: Ting, Robert C.

APPLICANT: Tham, Jill M.

TITLE OF INVENTION: Diagnosis of Parasites
FILE REPERENCE: 64-99

CURRENT APPLICATION NUMBER: U3/09/369,992C

CURRENT APPLICATION NUMBER: U999-06-06

PRIOR PILING DATE: 1998-02-05

PRIOR FILING DATE: 1997-09-05

PRIOR FILING DATE: 1997-09-05

PRIOR FILING DATE: 1997-04-21

PRIOR PELING DATE: 1997-04-21

PRIOR FILING DATE: 1997-04-21

PRIOR FILING DATE: 1997-04-21

PRIOR FILING DATE: 1997-04-21

PRIOR PELING DATE: 1997-04-21

PRIOR FILING DATE: 1997-04-21
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US-09-369-922-1
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US-09-369-992C-1
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Pricher, Dane K.

APPLICANT: Lalgudi, Raghuath V.
TITLE OF INVENTION: Mucleic Acid Sequences from Cyanidium caldarium and Uses;
TITLE OF INVENTION: thereof
TITLE OF INVENTION: thereof
TITLE OF INVENTION: 28-21 (15749)B
CURRENT APPLICATION NUMBER: US/09/540,235
CURRENT PILING DATE: 2000-04-03
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5333
LENGTH: 239
TYPE: Name
                                                               Sequence 4848, Application US/60128439
GENERAL INFORMATION:
APPLICANT: Fisher, Dane K.
APPLICANT: Flagudi, Raghunath V.
TITLE OF INVENTION: Uncleic Acid Sequences from Cyanidium caldarium and Uses TITLE OF INVENTION: thereof FILE REPREARCE: 38-21(15749) A CURRENT APPLICATION UNMER: US/60/128,439
CURRENT FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5661
EENGTH: 195
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Sequence 3158, Application US/60128439

Sequence 3158, Application US/60128439

Sequence 3158, Application US/60128439

APPLICANT: Fisher, Dane K.

APPLICANT: Lalgudi, Raghunath V.

TITLE OF INVENTION: UNcleic Acid Sequences from Cyanidium caldarium and Uses

TITLE OF INVENTION: Thereof

TILE REFERENCE: 38-21(15749)A

FILE REFERENCE: 38-21(15749)A

CURRENT APPLICATION UNMERR: US/60/128,439

CURRENT FILING DATE: 1999-04-06

NUMBER OF SEQ ID NOS: 5661
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Cyanidium caldarium
CYGANISM: Cyanidium caldarium
CTHER INFORMATION: Clone ID: LIB190-062-Q1-E1-E12
US-09-540-235-5333
                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: LIB190-062-Q1-E1-E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68;
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100.0%; Pred. No. 62;
:ive 0; Mismatches 0
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Best Local Similarity
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APPLICANT: Lalgudi, Raghunath V.
TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
TITLE OF INVENTION: ABOUT ACID ACID SEQUENCE:
CURRENT APPLICATION NUMBER: US/09/540,235
CURRENT FILING DATE: 2000-04-03
PRIOR PILING DATE: 2000-04-03
PRIOR FILING DATE: 60/128,439
PRIOR FILING DATE: 5674
SEQ ID NO 4801
LENGTH: 116
TYPE: N.
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Sequence 3619, Application US/60128439

Sequence 3619, Application US/60128439

SENERAL INFORMATION:
APPLICANT: Ladyadi, Raghunath V.
APPLICANT: Ladyadi, Raghunath V.
TITLE OF INVENTION: thereof
TITLE OF INVENTION: thereof
FILE REPRENCE: 38-21(15749)A

CURRENT APPLICATION NUMBER: US/60/128,439

CURRENT APPLICATION NUMBER: US/60/128,439

CURRENT PILING DATE: 1999-04-06

NUMBER OF SEQ ID NOS: 5661

LENGTH: 108
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                                                                                                                                                     Query Match 100.0%; Score 21; DB 19; Length 5849; Best Local Similarity 100.0%; Pred. No. 5.5; Matches 21; Conservative 0; Mismatches 0; Indels 0;
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68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-049-Q1-E1-B2
US-60-128-439-3619
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                                                             TYPE: DNA; Plasmodium berghei US-09-369-992C-1
SOFTWARE: Patentin Ver. 2.0
                       SEQ ID NO 1
LENGTH: 5849
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137 GTGCCAGCAGCAGCGGTAA 155
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Best Local Similarity
Matches 19; Conserva
                                                       RESULT 11
US-60-128-439-1486
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APPLICANT: Lalgudi, Raghunath V.

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

THE REPERBACE:

CURRENT APPLICATION NUMBER: US/09/540,235

CURRENT FILING DATE:

PRIOR APPLICATION NUMBER: US/09/540,235

PRIOR FILING DATE:

1999-04-06

SEQ ID NOS:

5674
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GENERAL INFORMATION:
APPLICANT: Fisher.
APPLICANT: Fisher.
APPLICANT: Lalgudi, Raghunath V.
TITLE OF INVENTION: Nacleic Acid Sequences from Cyanidium caldarium and Uses;
TITLE OF INVENTION: thereof
TITLE REFERENCE: 38-21(15749)4
CURRENT APPLICATION NUMBER: US/60/128,439
CURRENT FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5661
SEQ ID NO 2099
LENGTH: 287
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61;
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Pred. No. 61;
                                                                                                                                                                                          0; Indels
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                                                                                          ; OTHER INFORMATION: Clone ID: LIB190-043-Q1-E1-C12
US-60-128-439-3158
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US-60-128-439-2909
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OCGANISM: Cyanidium caldarium
CTHER INFORMATION: Clone ID: LIB190-019-Q1-E1-H1
US-09-540-235-1015
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100.0%; Pred. No. c...
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Best Local Similarity 100.0%; P.
Matches 19; Conservative 0;
                                    TYPE: DNA ORGANISM: Cyanidium caldarium
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ORGANISM: Cyanidium caldarium
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Best Local Similarity 100 (
Matches 19; Conservative
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US-09-540-235-1015
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US-60-128-439-2909
SEQ ID NO 3158
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Sequence 4526, Application US/09540235
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
Injury Nucleic Acid Sequences from Cyanidium caldarium and Uses
TITLE OF INVENTION:
TOTAL OF INVENTION:
TOTAL OF INVENTION:
TOTAL OF INVENTION NUMBER: US/09/540,235
CURRENT FILING DATE: 2000-04-03
PRIOR PELICATION WUMBER: 1999-04-06
PRIOR PELICATION WUMBER: 5674
SEQ ID NOS: 5674
SEQ ID NOS: 5674
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APPLICANT: Lalgudi, Raghuath V.
TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
TITLE OF INVENTION: thereof
FILE REPERENCE: 38-21(15749)B
CURRENT APPLICATION NUMBER: US/09/540,235
                                                      APPLICANT: Fisher, Dane K.
APPLICANT: Fisher, Dane K.
APPLICANT: Lalgradi, Raghumath V.
TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
TITLE OF INVENTION: thereof
FILE REPERENCE: 38-21(15749)A
CURRENT APPLICATION NUMBER: US/60/128,439
CURRENT FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5661
LENGTH: 295
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Pred. No. 61;
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CRGANISM: Cyanidium caldarium

CTHER INFORMATION: Clone ID: LIB190-040-Q1-E1-B11

US-09-540-235-4526
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OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB190-019-01-B1-H1
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Sequence 1486, Application US/60128439 GENERAL INFORMATION:
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Best Local Similarity 100.0%; P. Matches 19; Conservative 0;
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ORGANISM: Cyanidium caldarium
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US-09-540-215-4659

US-09-540-215-4659

Sequence 4659, Application US/09540235

GENERAL INPORMATION:
APPLICANT:
TITLE OF INVENTION:
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US-60-128-439-5580
US-60-128-439-5580
Sequence 5580, Application US/60128439
GENERAL INFORMATION:
APPLICANT: Fisher, Dane K.
APPLICANT: Lalgudi, Raghunath V.
TITLE OF INVENTION: Uncled Acid Sequences from Cyanidium caldarium and Uses
TITLE OF INVENTION: Lhereof
TITLE OF INVENTION: Lhereof
TITLE OF INVENTION UNCLES: US/60/128,439
CURRENT APPLICATION NUMBER: US/60/128,439
NUMBER OF SEQ ID NOS: 5661
SEQ ID NOS: 5661
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90.5%; Score 19; DB 68; Length 301;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels
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90.5%; Score 19; DB 23; Length 302;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels
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90.5%; Score 19; DB 23; Length 301;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels
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CSGANISM: Cyanidium caldarium
CTHER INFORMATION: Clone ID: LIB190-043-Q1-E1-C12
US-09-540-235-4659
                                                                                                                                                                                                                                                         TYPE: DNA

OCGANISM: Cyanidium caldarium

OTHER INFORMATION: Clone ID: LIB190-071-Q1-E1-G6
US-09-540-235-3580
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US-60-128-439-5580
                                                     60/128,439
                                                                           1999-04-06
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CURRENT FILING DATE: 2000-
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 3580
LENGTH: 301
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Search completed: August 4, 2004, 11:29:59 Job time: 1918.07 secs

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FEATURE:
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                                                                                                                                                          August 4, 2004, 06:01:54; Search time 37.9518 Seconds (without alignments) 307.073 Million cell updates/sec
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Sequence 2,
Sequence 1,
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-621-976-9153
US-09-621-976-9153
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US-09-252-991A-1179
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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No.
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RESULT 2
US-09-328-252-2320
US-09-328-352-2320

Sequence 2320, Application US/09328352

Patent No. £56258.

GENERAL INFORMATION:

APPLICANT: GARY L. Breton et al.

TITLE OF INVENTION: BUTCHOL AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC99-03PA

CURRENT PELLIAGIATION WHBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

LENGTH: 684

TYPE: DNA
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Sequence 7151, Application US/09252991A

Beach No. 6551795

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION UNMER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

FRIOR APPLICATION NUMBER: US 60/074,788

FRIOR FILING DATE: 1998-02-18

FRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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COTHER INFORMATION: Identity of nucleotide at the above locations are unknown. US-09-252-991A-7151
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                 Sequence 538, App
Sequence 181, App
Sequence 1810, App
Sequence 3580, App
Sequence 9123, App
Sequence 9123, App
Sequence 1658, App
Sequence 10011, App
Sequence 2659, App
Sequence 2659, App
Sequence 2659, App
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15946, A
156, App
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Sequence Sequence Sequence
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               US-09-621-976-539
US-09-621-976-539
US-09-621-976-3580
US-09-621-991A-606
US-09-252-991A-9188
US-09-252-991A-9188
US-09-252-991A-9188
US-09-252-991A-16653
US-09-252-991A-10011
US-09-621-976-3656
US-09-621-976-3656
US-09-681-976-3656
US-09-489-039A-1151
US-09-489-039A-1151
US-09-489-039A-1151
US-09-252-991A-1151
US-09-489-039A-1151
US-09-252-991A-1151
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ORGANISM: Pseudomonas aeruginosa
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76.2%; SCC.
100.0%; Pre
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Best Local Similarity 100.0
Matches 16; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                                    Conservative
                                      Local Similarity
nes 16; Conserv
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NAME/KEY: unsure
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                   Query Match
Best Local &
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Sequence 7209, Application US/09252991A

Sequence 7209, Application US/09252991A

Sequence 7209, Application US/09252991A

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILLING DATE: 1999-02-18

PRIOR FILLING DATE: 1999-02-18

PRIOR FILLING DATE: 1999-02-18

PRIOR FILLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 7209

LENGTH: 2541
                                                                                                                                                                                                                                                                                                                                                     US-09-252-991A-7428/C

| Sequence 7428, Application US/09252991A
| Sequence 7428, Application US/09252991A
| Sequence 7428, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION:
| APPLICANT MARC J. Rubenfield et al.
| TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| CURRENT APPLICATION NUMBER: US 60/074,788
| PRIOR PILING DATE: 1998-02-18
| PRIOR PELICATION NUMBER: US 60/094,190
| PRIOR PILING DATE: 1998-02-18
| CONTINUENCE OF SEQ ID NOS: 33142
| CONTINUENCE OF SEQ ID NOS: 33142
| CONTINUENCE OF SEQ ID NOS: 33142
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NAME/KEX: unsure
LOCATION: (2058)
COTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7209
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, OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7428
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                                                                                               Query Match 76.2%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 10; Matches 16; Conservative 0; Mismatches
                     , ORGANISM: Acinetobacter baumannii
US-09-328-352-2320
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity
Trahes 16; Conserve
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NAME/KEY: unsure
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Patent No. 6653118
GENERAL INFORMATION:
APPLICANT: Tanuma, Sei-ichi
APPLICANT: Tanuma, Sei-ichi
APPLICANT: Tanuma, Sei-ichi
APPLICANT: Shiokawa, Daisuke
TITLE OF INVENTION: No. 6653118el Deoxyribonuclease, Gene Encoding Thereof and Use Th
TITLE OF INVENTION: No. 6653118el Deoxyribonuclease, Gene Encoding Thereof and Use Th
TITLE OF INVENTION: NOWBER: US/09/807,784B
CURRENT FILING DATE: 1999-08-17
NUMBER OF APPLICATION NUMBER: UP 11-230870
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 15
LENGTH: 32
TYPE: DNA
CORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1117); OTHER INFORMATION: Identity of nuclectide at the above locations are unknown.
US-09-252-991A-7487
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ore 16; DB 4; Length 2541;
red. No. 10;
Mismatches 0; Indels
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100.0%; Pred. No. 33;
cive 0; Mismatches 0; Indels
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 Score 16;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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US-09-152-991A-1269/C

is Sequence 1269, Application US/09252991A

is TITLE OF SETTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

is TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

is TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

is CURRENT APPLICATION NUMBER: US/09/252,991A

is CURRENT FILING DATE: 1998-02-18

is PRIOR FILING DATE: 1998-02-18

is PRIOR FILING DATE: 1998-07-27

is SEQ ID NOS: 33142

is ENGTH: 1050
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Patent No. 6610836

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
PREDICANT:
TITLE OF INVENTION:
PREDICANT:
TITLE OF INVENTION:
TITLE REPRESENCE: 2799.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 1990-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
SPRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 4976
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                                                                                                                                                                                        Length 558;
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                                                                                                                                                                                        71.4%; Score 15; DB 4;
100.0%; Pred. No. 32;
tive 0; Mismatches
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US-09-252-991A-1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Klebsiella pneumoniae
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 958
LENGTH: 558
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                          ; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-958
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US-09-489-039A-4976
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                                                                                                                                                  APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE BOR INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBACE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 1498
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Sequence 958, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 2709, 2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
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Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Unmas Milne Edwards, J.B.
APPLICANT: JODert, S.
TITLE FERENCE: GENSET. 054PR2

CURRENT APPLICATION UNBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SEQ ID NO 9153

LENGTH: 398
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                                                                                          5-09-540-236-1498/c
Sequence 1498, Application US/09540236
Patent No. 6673910
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LOCATION: 320
OTHER INFORMATION: n=a, g, c or t
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  32 TGCCAGCAGCAGCGG 18
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Matches 15; Conservative
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, ORGANISM: M.catarrhalis
US-09-540-236-1498
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US-09-621-976-9153/c
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                                                                                                        DB 3; Length 1575;
32;
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                                                                                                                                                                       0; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US/09/861,034B
FILING DATE: 18-May-2001
CLASSIFICATION NUMBER: 08/639294
APPLICATION NUMBER: 08/639294
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: JOHNSTON: SEAR. 1996
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 35,910
REFERENCE/DOCKET NUMBER: 35,910
REFERENCE/DOCKET NUMBER: 35,010
REFERENCE/DOCKET NUMBER: 35,010
REFERENCE/DOCKET NUMBER: 35,010
REFERENCE/DOCKET NUMBER: 35,010
REFERENCE/SOCKET NUMBER: 35,010
REFERENCE/S
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100.0%; Pred. No. 52,
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-09-861-034B-1/C
Sequence 1, Application US/09861034B
Fatent No. 6569429
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
TITLE OF INVENTION: Human DNase II
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                              71.4%; Score 15; DB 100.0%; Pred. No. 32; ive 0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-861-034B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence I, Application US/09147915A Patent No. 6184034 GENERAL INFORMATION:
APPLICANT: Eastman, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1575 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                         106 receaecacece 92
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                                                                                  Query Match
Best Local Similarity 10v...
Best Local Similarity 10v...
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Best Local Similarity 100.
Matches 15; Conservative
                      , MOLECULE TYPE: DNA
US-08-639-294-1
   Linear
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US-09-147-915-1/c
TOPOLOGY:
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                                                                                                                        US-09-252-991A-1179/C

i Sequence 1179, Application US/09252991A

sequence 1179, Application US/09252991A

patent No. 6551795

i CHERRAL INFORMATION:

APPLICANT: Marc J WIDENTION:

APPLICANT: Marc J WIDENTION:

TITLE OF INVENTION: ARUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1179

LINGTH 1308
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Will F.
ITILE OF INVENTION: Human DNase II
NUMBER OF ENGUNICES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genericeh, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
COUNTRY: USA
ZIP: 94080
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SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,294
FILING DATE: 25-Apr-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JOHNSTON, Sean A.
REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: 91024
TELECHOME: 415/225-3862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-639-294-1/c; Sequence 1, Application US/08639294; Patent No. 6265195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1179
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                               818 CCAGCAGCAGCGGTA 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 71.4
Best Local Similarity 100.
Matches 15; Conservative
LENGTH: 1575 base | TYPE: Nucleic Acid
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APPLICANT: Krieser, Ronald
TILE REPERENCE: DC-0097
FILE REPERENCE: DC-0097
CURRENT APPLICATION NUMBER: US/09/147,915A
CURRENT PILING DATE: 1999-03-23
EARLIER APPLICATION NUMBER: PC7/US97/18262
EARLIER APPLICATION NUMBER: 60/028,539
EARLIER APPLICATION NUMBER: 60/028,539
EARLIER PILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 18
SEQ ID NO!
SEQ ID NO!
LENGTH: 1915
CONGANISM: Home sapiens
US-09-147-915-1
Query Match
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
Oy
Search completed: August 4, 2004, 09:23:34
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EMERATYOLS, Fungli, Ascomycota, Pezizomycotina, Eurotiomycetes, Buraryota, Fungli, Ascomycota, Pezizomycotina, Eurotiales, Trichocomaceae; Emericella.

Eurotiales, Trichocomaceae; Emericella.

(Bases 1 to 213)

Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Prade, R. and Roe, B.

An Aspergillus nidulans EST Database

Unpublished (1998)

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the CDNA clones to the Fungal
Genetics Stock Center
                                            BIG97005 [K52e10.7]
BIG97004 [K52e10.7]
BIG97004 [K52e10.7]
BIG96309 [C41d00.7]
BIG96309 [K50e0.7]
BIG96309 [K50e0.7]
BIG96309 [K50e0.3]
BIG96007 [K50e0.7]
BIG96007 
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BIT53233
BIT02033
BIR06203
BIR066073
BIR06073
BIR060773
CB081772
AW381773
BIR708185
BIR708185
BIR91155
AW1353986
AW077500
BW077610
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CB678345
BZ067695
BZ067695
CD857812
CD85759
CD857943
CD8582
CD856671
CD856671
CD856671
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BI897004
AA784579
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                                                     RESULT 1
AI212321/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
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AUTHORS
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BF064383 SWOVAFCAP
AIS85049 fb69g07.x
AI211182 00c05a1.f
                                                                                                                                                                                  2004, 05:41:25; Search time 1532.58 Seconds (without alignments) 428.668 Million cell updates/sec
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Compugen Ltd
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                           GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                               22
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                                                                                                                                   OM nucleic - nucleic search, using sw model
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BF064383
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Gapop_60.0 , Gapext 60.0
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em_esthum:...
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Maximum DB seq length: 200000000
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Match Length DB
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Danio rerio
                                                                           Query Match
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AI585049/c
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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                             ORIGIN
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                                                                                                                                                                                                             /tissue_type="vegetative mycelia, asexual structures"
/clone_lib="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/note="Vector: pBlueScript SN-; Site_l: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into "XhoI site of pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Onchocerca volvulus
Onchocerca volvulus
Eukaryota, Metazoa, Nematoda, Chromadorea, Spirurida, Filarioidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF064383
SWOVAFCAP48BIISK Onchocerca volvulus adult female cDNA
(SAN98MIW-OVAF) Onchocerca volvulus cDNA clone SWOVAFCAP48BII 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ontract: Steeving williams

Contract: Steeving Williams

Molecular Parasitology
Smith College Department of Biological Sciences

Smoth College Department of Sciences, Clark Science Center, Smith

College, Northampton, MA, 01063, USA

Tel: 4135853786

Fax: 4135853786

Email: genome@smith.edu

Seq primer: pBluescript SK.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Onchocercidae, Onchocerca.

1 (Dases 1 to 258)
Lizotte-Wanlewski,M. and Williams,S.A.

Genes expressed in adult female stage of Onchocerca volvulus Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev stage="adult"
/lab_host="XL1-Blue MRF'"
/clone lib="Onchocerca volvulus adult female cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                 72.7%; Score 16; DB 9; Length 213; 100.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                 /organism="Emericella nidulans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Onchocerca volvulus"
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Preq. ...
                                                                                                                                                                      /db_xref="taxon:162425"
/clone="x2g02a1"
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/sex="female"
Seq primer: M13-20
High quality sequence stop: 88.
Location/Qualifiers
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/db_xref="taxon:6282"
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/strain="FGSC A26"
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Danio Terio
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Danio Danio
Cyprinidae; Danio.

Cypriniformes; Cyprinidae; Danio.

I (Dases I to 262)
Eddy, S., Hillier, L., Enbrach, H., Lee, R., Li, F., Marra, M.,
Eddy, S., Hillier, L., Kucha, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., NcCann, R.,
Waterston, R. and Wilson, R.
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Hal: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
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Fax: Jat 286 1800
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Eb69g07.XI Zebrafish WashU MPING EST Danio rerio cDNA clone
MAMCE:3717180 3', mRNA sequence.
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zebrafish identity (p-value greater than 1e-99) found to:
gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
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from Dr.Steven A. Williams, email: genome@smith.edu."
                                                                                                                                                                                        Gaps
                                                                                                                                                                                        .;
0
                                                                                                      Length 258;
                                                                                                                                                                                    0; Indels
                                                                                                             10;
                                                                                                          ore 16; DB 1
red. No. 32;
Mismatches
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/lab_host="XL1-blue MRF"
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                                                                                                             Score 16;
Pred. No.
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High quality sequence stop: 254
POLYA=No.
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/db_xref="taxon:7955"
/clone="IMAGE:3717180"
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100.0%; Pre
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                                                                                                             72.78;
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Matches 16; Conservative
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mRNA sequence.
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AA497171/c
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AI381122/c
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/moltype="mmkn"
/strain="FGSC A26"
/db xref="texon:162425"
/clone="conservation of the properties of the
analysis were selected following oligonuclectide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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We anticipate the future release of the CDNA clones to the Fungal
Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Prade, R. and Roe, B.
An Aspergillue nidulans BST Database
Unpublished (1998)
Other_ESTS: 00c05al.rl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OX 73019, USA
Tel: 405 325 4912
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Emericella nidulans
Euraryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, Emericella.

1 (bases 1 to 285)
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High quality sequence stop: 219.
Location/Qualifiers
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AI211182.1 GI:3773124
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Matches 16; Conserv
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EST 26-JAN-1999
CDNA
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Xho I; Filarial nematcde parasite of humans. Two adult—
female worms of Onchocerca volvulus were isolated from
consenting patients and quick frozen. Adult female mRNA
was converted to double-stranded cDNA using reverse
transcriptase and oligo(dT) followed by RNase H and DNA
pol I. The library has 7 x 10E5 independent recombinants
and the average riser size is ~1100bp. The library was
constructed by Michelle Lizotte-Waniewski with worms
provided by Dr. Sara Lustigman. The library is available
from Dr.Steven A. Williams, email: genome@smith.edu."
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                                                                                                                                                                                                                                                                       Eukaryota, Metacada, Nematoda, Chromadorea, Spirurida, Filarioidea, Onchocercidae, Onchocerca.

(I basea 1 to 334)

Lizotte-Maniewski, M. and Williams, S.A.
Genes expressed in adult female stage of Onchocerca volvulus (Unpublished (1998))

Contact: Steven A. Willams
Molecular Parasitology
Smith College Department of Biological Sciences
Smith College Department of Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
AI381122 SWOVAFCAP30F01SK Onchocerca volvulus adult female cDNA (SAN98MIM-OVAF) Onchocerca volvulus cDNA clone SWOVAFCAP30F01 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Danio rerio (zebrafish)
Danio rerio
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/lab_host="XLi-Blue MRF'"
/clone lib="Onchocerca volvulus adult female cDNA
(SAW98MLW-OvAF)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOAFCAF30F01"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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Onchocerca volvulus
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Best Local Similarity 100.
Matches 16; Conservative
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Washington University School of Medicine
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BI897004
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Best Local Similarity
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled 26-somite embryos"
/lab host="mixed"
/lab host="xil-blue MRF"
/clon=lib="Zebrafish ICRFzfls"
/clon=strand cDNA was primed with a Not I - oligo(dT)15 primer
[5:padrAGTTCARAGAGGGGGCCCTTTTTTTTTTTTTTTT], on
mRNA from pooled 26 somite zebrafish embryos;
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPOTT vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRF, London and Max
Planck Institut fuer Molekulare Genetik, Berlin) and was
not biochemically normalised. 70,000 clones from this
library were arrayed on high density filters and
subsequently screened by oligomucleotide hybridization
fingerprinting to identify unique or minimally redundant
clones for more intensive analysis."
                                                                                                                                                                                                              Contact: Steve Johnson
Washington University School of Medicine
4444 Porest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: esr@watson.wustl.edu
Steve Johnson lab internal ID - Pl 89 NOTE - For this library, the CLONE id field represents a position identifier on the original clow. Library preparation plate. CDNA Library Preparation: Matthew Clark: CDNA Library Arrayed by: Matthew Clark: DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, and Max Planck Institut fuer Molekulare Genetik, Berlin Tel 449 30 84 13 1235
Seq primer: -40ml3 ET from Amersham
High quality sequence 500: 315.
          Clark, M., Lehrach, H., Appel, B., Eisen, J., Johnson, S., Marra, M., Bady, S., Hilliar, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Schellenberg, K., Steptoe, M., Le, N., Lennon, G., Martin, J., Moore, B., Wylie, T., Mereston, R. and Wilson, R., Maretish Est Project Unpublished (1997)
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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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  Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="3D9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="mixed"
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BI897005
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Best Local S
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JOURNAL
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Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Stepter,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,W., Schurk,R.,
Watter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Watterston,R. and Wilson,R.
Watterston,R. and Wilson,R.
Unpublished (1998)

U Opther Ests (Efselo.)
Concact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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SM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

El (bases 1 to 371)

S Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Washy Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: zbrafish@watson.wustl.edu
Library constructed by: Bernhard Korn DNA Sequencing by: Washington
University Genome Sequencing Center Clone distribution:
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zebrafish identity (p-value greater than 1e-99) found to:
gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
rerio cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E.Coli (DHIOB/XL2blue)"
/clone_lib="Zebrafish_15-19hr embryonic_cDNA"
/note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; This
Zebrafish library was constructed by Dr. Bernhard Korn
(email: b.korn@dkfz-heidelberg.de): RZFD library number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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/lab_host="E.Coli (DH10B/XL2bl)
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Location/Qualifiers
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/strain="unspecified"
/db_xref="taxon:7955"
/sex="mixed"
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Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI897004.1 GI:16140140
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Conservative
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                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                          16;
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BI896339/c
                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                         ORIGIN
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                                                                                                                                                                                                                                                                                       /organ.sm="Danio rerio"
/organ.sm="Danio rerio"
/mol type="mRNA"
/strain="unspecified"
/db xref="taxon:7955"
/sex==mixed"
/lab_host="E.Coli (DH10B/XL2blue)"
/lab_host="E.Coli (DH10B/XL2blue)"
/lab_host="E.Zobrafish 15-19hr embryonic cDNA"
/lone lib="Zebrafish 15-19hr embryonic cDNA"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This Zebrafish library was constructed by Dr. Bernhard Korn (email: b.korn@dkfz-heidelberg.de). RZPD library number: 717"
                                                      Email: zbrafish@watson.wustl.edu
Library constructed by: Bernhard Korn DNA Sequencing by: Washington
University Genome Sequencing Center Clone distribution:
RessourcenZentrumprimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                  zebrafish identity (p-value greater than 1e-99) found to:
gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
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flh09al.fl Aspergillus nidulans 24hr asexual developmental and
vegetative cDNA lambda zap library Emericella nidulans cDNA clone
flh09al 3', mRNA sequence.
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Emericella nidulans
Eurayota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.

(bases 1 to 377)

Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe,B.
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Bruce A. Koe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry.
Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA
Fat: 405 325 4912
Fax: 405 325 7762
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: broe@ou.edu
We anticipate the future release of
Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="flh09a1"
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Location/Qualifiers
                                                                                                                                                                                                                               Seq primer: T7 from Gibco.
Location/Qualifiers
1. .371
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AA784579.1 GI:2844747
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Best Local Similarity 100.
Matches 16; Conservative
                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                               rerio cDNA
                                                                                                                                                  www.rzpd
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Danjo Perilo

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

Sclark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,

Bady,S., Hillier,L., Kacaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising, A. Allen,M., Bowers,Y.,

Ritter,P., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

Wather,P., and Wilson,R.

Washler,T., and Wilson,R.

Unpublished (1998)

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Fax: 314 286 1810

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CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Washington University Genome

Sequencing Center Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) email context: info@genomesystems.com) and Research Genome Systems; Com) and Research Genome Systems; com) email context: info@genomesystems.com) (email contex
/tissue type="vegetative mycelia, asexual structures" /clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library" /note="Vector: pBlueScript SK-; Site_l: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6-4302.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone (RMGE:3724131 3', mRNA sequence.
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gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
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                                                                                                                                                                                                                                                                                                                             Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                        DB 9;
34;
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/organism="Danio rerio"
/nol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3724131"
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Pred. No.
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High quality sequence stop: 4
Location/Qualifiers
                                                                                                                                                                                                                                                                                       72.7%; SCOL.
100.0%; Pre
0;
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us-09-940-860-3.oligo.rst

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double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the DSPORTI vector (BRL). Library was constructed by Matthew clark (Lahrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following obligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data ware used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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E (Wases I to 445)
S Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Ghibons,M., Pape,D., Harvey,N., Schurk,R., Watter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Washu Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
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CDNA Library Preparation: John Ngai. cDNA Library Arrayed by:

Authew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

Info@genomesystems.com) and Research Genetics, Hustosille, Alabama

(web address: www.resgen.com) (email contact: info@cespen.com) and

RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.7%; Score 16; DB 12; Length 445; 100.0%; Pred. No. 35; ive 0; Mismatches 0; Indels
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Putative full length read
The vector to vector length is 522
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/db_xref="taxon:7955"
/clone="IMAGE:5386907"
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Location/Qualifiers
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Danio rerio
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Best Local Simi
Matches 16;
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BM156391/c
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/sex="mixed male and female"

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7el: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 61800
Fax: 316 286 61800

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fr79a06.x1 zebrafish adult brain Danio rerio cDNA clone
IMAGE:4966930 3', mRNA sequence.
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zebrafish identity (p-value greater than 1e-99) found to:
gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
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Catinopterygii, Neopterygii, Teleostel, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
(pases 1 to 448)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                       /dev_stāge="adult"
| Aab host="B. coli DH10B"
| Alab host="B. coli DH10B"
| Alab host="Vector: pZIPLOX; Site_1: Not1; Site_2: Sal1;
| Anote="Vector: pZIPLOX; Site_1: Not1; Site_2: Sal1;
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/tissue_type="brain"
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High quality sequence stop: 408.
Location/Qualifiers
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/db_xref="taxon:7955"
'tissue_type="brain"
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100.0%; Preć
0; M
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Danio rerio
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Best Local Similarity
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BI533213/c
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AUTHORS
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KEYWORDS
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
7el: 314 286 1810
Fax: 314 286 1810
Email: abrafish@watson.wustl.edu
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing By: Washington University Genome
Sequencing Center Clone distribution: Genome Systems. St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@espsrems.com) and Research Genetics Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@eresgen.com)
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                               MN102203 452 bp mRNA linear EST 26-JUL-2002 fv14d10.x1 zebrafish adult brain Danio rerio cDNA clone IMAGE:5386435 3', mRNA sequence.
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gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRPzfls Danio
rerio cDNA
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1 (Dases 1 to 452)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
WashU Zebrafish EST Project 1998
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/lab host="E. coli DH10B"
/lone=lib="zebrafish adult brain"
/note="voctor: pZIPLOX; Site 1: Not!, Site 2: Sall;
Original library was constructed in lambdaZIPLOX. M
exclaion of the cDNA library was performed to yield
pZIPLOX plasmids. Insert check was done in original
library.
Original library was constructed in lambdazIPLOX. Peccision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library.
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                                                                                                                                                            DB 12; Length 448; 35;
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/tissue_type="brain"
                                                                                                                                                         72.7%; Score 16; DB 100.0%; Pred. No. 35; Live 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:7955"
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Location/Qualifiers
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                                                                                                                                                                                     Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                 Query Match
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BM102203/c
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AUTHORS
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ORIGIN

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Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neoperygii; Teleostei; Ostariophysi; Cyrinidae; Danio.

[ Cyriniformes: Cyrinidae; Danio.

[ Lark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kacaba,T., Marthi,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Schn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., WashU Zebrafish EST Project 1998

L. Unpublished (1998)

Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Fax: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: zbrafish@watson.wustl.edu
Library constructed by: Bernhard Korn DNA Sequencing by: Washington
University Genome Sequencing Center Clone distribution:
RessourcenZentrumPrimarPatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zebrafish identity (p-value greater than 1e-99) found to:
gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
rerio cDNA
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k50e03.x1 Zebrafish 15-19hr embryonic cDNA Danio rerio cDNA 3',
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/lab_host="E.Coli (DH10B/XL2blue)"
/clone lib="Zebrafish 15-19hr embryonic cDNA"
/note="Vector: pSPORTI; Site_1: NotI; Site_2: SalI; This Zebrafish library was constructed by Dr. Bernhard Korn (email: b.korn@dkfz-heidelberg.de). RZPD library number:
                                                               Gaps
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Pred. No. 36;
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Mismatches
                                                               Mismatches
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Location/Qualifiers
                      Score 16;
Pred. No.
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/strain="unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:7955"
/sex="mixed"
         72.7%; SCOL.
100.0%; Pre
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100.0%; Pre
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Matches 16; Conservative
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us-09-940-860-3.0ligo.rst

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BI708149 452 Pp mRNA linear EST 19-SEP-2001 fs42g04.x1 Zebrafish adult olfactory Danio rerio cDNA clone IMAGE:5070534 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www.rzpd.de)
Sebrafish identity (p-value greater than le-99) found to:
gi[2230492]gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
rerio cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tiscue type="Olfactory rosettes"
/tashuse type="olfactory rosettes"
/lab_hose="adult" (disco BRL)"
/clone lib="zebrafish adult olfactory"
/note="Vector: pSPORT1; Site 1: Not1; Site 2: Sal1; This is a directionally cloned cDNA library from adult
Zebrafish olfactory epithelium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.7%; Score 16; DB 12; Length 459; 100.0%; Pred. No. 36; 0; Indels cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5070534"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 440.
Location/Qualifiers
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                                                                                BI708149.1 GI:15683844
                                                                                                             Danio, rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="mixed"
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Best Local Similarity 100.
Matches 16; Conservative
RESULT 15
BI708149/c
                                                                  ACCESSION
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KEYWORDS
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                                        DEFINITION
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AUTHORS
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Gaps

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Search completed: August 4, 2004, 09:20:54 Job time : 1535.58 secs

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August 4, 2004, 04:00:30 ; Search time 164.337 Seconds (without alignments) 517.009 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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geneseqn2001as:\* geneseqn2003bs:\* geneseqn2003cs:\* geneseqn2001bs:\* geneseqn2003as:\* geneseqn2004s:\* geneseqn1990s:\* geneseqn2000s:\* geneseqn2002s 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Aaa37798 Helicobac	Aaa37797 Helicobac	Aaa37796 Helicobac	Aaa37795 Helicobac	Aaa37794 Helicobac	Aaa37793 Helicobac	Aaa37791 Helicobac	Aav66849 Chlamydia	Aav66846 Chlamydia	Aav66848 Chlamydia	Aav66845 Chlamydia	Aav66850 Chlamydia	Aav66847 Chlamydia	Aas11031 Chlamydia		Aah28376 Intergeni	Aah28407 Intergeni	Continuation (7 of	Continuation (11 o	Abz34685 Coding se	Aca30087 Prokaryot	Ada69779 Rice gene	Aas46575 Tumour su
SUMMARIES	qi		AAA37798	AAA37797	AAA37796	AAA37795	AAA37794	AAA37793	AAA37791	AAV66849	AAV66846	AAV66848	AAV66845	AAV66850	AAV66847	AAS11031	AAV66851	AAH28376	AAH28407	AAZ01425 06	AAX91990_10	ABZ34685	ACA30087	ADA69779	AAS46575
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	24	25	Ñ	N				c 31	32	33	34	c 35	36	37	38	39	40	41	c 42	c 43	44	45

## ALIGNMENTS

RESULT 1

Post-processing: Listing first 45 summaries

N\_Geneseq\_29Jan04:\* 1: geneseqn1980s:\*

Database :

16SrRNA; detection; strain identification; gastric ulcer; Van Doorn L; Quint W, Helicobacter 16SrRna DNA sequence R28TOTAAL Haesebrouck F, AAA37798 standard; DNA; 1172 BP. chronic gastritis; zoonoses; ss. Candidatus Helicobacter bovis. 99EP-00870035. 99EP-00870035. De Groote D, (revised)
(first entry) WPI; 2000-559879/52. (UYGE-) UNIV GENT. Helicobacter; Ducatelle R, EP1035219-A1 25-FEB-1999; 25-FEB-1999; 15-SEP-2003 15-JAN-2001 13-SEP-2000 AAA37798; AAA37798 

Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or primers for detecting and/or typing Helicobacter strains present in a biological sample.

Claim 2; Page 24-25; 132pp; English.

This sequence represents a Helicobacter 16SrRNA sequence of the invention. A probe which specifically hybridises to the 16SrRNA sequence and a primer which specifically maplifies it are used for detecting and/or typing Helicobacter strains present in a biological sample (obtained from mammals preferably oattle and pigs) by hybridishig or specifically amplifying the 16S rRNA gene target region of Helicobacter strains present in the biological sample with the primer or probe, respectively. The 16S rRNA sequence is also used as a medicament. The 16S rRNA sequences are used for studying and detecting pathogenic Helicobacter strains which cause gastric ulcers and chronic gastritis in

1035 GGAGGAAGGCGAGGATGACG 1054

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AAA37796 standard; DNA; 1236

RESULT 3

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mammals, particularly cattle and pigs. The method is also useful for detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated 168 rDNA Helicobacter polynucleotides useful as probes primers for detecting and/or typing Helicobacter strains present in a biological sample.
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llarity 100.0%; Pred. No. 0.34;
Conservative 0; Mismatches 0; Indels 0
                                                                                                      Query Match
100.0%; Score 20; DB 3; Length 1172;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels (
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                                                                         Sequence 1172 BP; 323 A; 259 C; 345 G; 245 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter 16SrRna DNA sequence R27TOTAAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Groote D, Haesebrouck F,
                                                                                                                                                                                                    GGAGGAAGGCGAGGATGACG 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 24; 132pp; English.
                                                                                                                                                                                 1 GGAGGAAGGCGAGGATGACG 20
                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candidatus Helicobacter bovis.
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(first entry)
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15-JAN-2001
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invention. A probe which specifically hybridises to the 16SzRNA sequence and a primer which specifically maplifies it are used for detecting and/or typing Helicobacter strains present in a blological sample (obtained from mammals preferably cattle and pigs) by hybridising or specifically amplifying the 16S rRNA gene target region of Helicobacter strains present in the biological sample with the primer or probe, respectively. The 16S rRNA sequence is also used as a medicament. The 16S rRNA sequences are used for studying and detecting pathogenic Helicobacter strains which cause gastric ulcers and chronic gastritis in mammals, particularly cattle and pigs. The method is also useful for detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise OS field)
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                                                                                                                 Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated 168 rDNA Helicobacter polynucleotides useful as probes primers for detecting and/or typing Helicobacter strains present in a
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                                                                                                                                                                                                                                                                                                                                                 Van Doorn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents a Helicobacter 16SrRNA sequence of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1236 BP; 336 A; 271 C; 369 G; 259 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                 Quint W,
                                                                                      Helicobacter 16SrRna DNA sequence R13D001INV
                                                                                                                                                                                                                                                                                                                                                 Haesebrouck F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 23-24; 132pp; English.
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                                                                                                                                  chronic gastritis; zoonoses; ss.
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                                                                                                                                                                   Candidatus Helicobacter bovis.
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Best Local Similarity
Then 20; Conserve
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                                         15-SEP-2003
15-JAN-2001
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15-JAN-2001
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                AAA37796;
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1 GGAGGAAGGCGAGGATGACG 20

Query Match Best Local Similarity

Matches

Ducatelle R,

25-FEB-1999;

EP1035219-A1

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This sequence represents a Helicobacter 16SrRNA sequence of the invention. A probe which specifically hybridises to the 16SrRNA sequence and a primer which specifically maplifies it are used for detecting and/or typing Helicobacter strains present in a biological sample (obtained from mammals preferably cattle and pigs) by hybridising or specifically amplifying the 16S rRNA gene target region of Helicobacter strains present in the biological sample with the primer or probe respectively. The 16S rRNA sequence is also used as a medicament. The 16S rRNA sequence is also used as a medicament. The 16S rRNA sequence is also used as an edicament. The 16S rRNA sequence is also used as an edicament, the 16S rRNA sequence is also used as an edicament, or an endicament, and obtains and chronic gastricis in mammals, particularly cattle and pigs. The method is also useful for detection of zonoses in humans. (Updated on 15-SEP-2003 to standardise
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                                                                                                                                                                                                Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or primers for detecting and/or typing Helicobacter strains present in a biological sample.
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                                                                                                            Van Doorn L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Van Doorn L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 3; Length 1299; 100.0%; Pred. No. 0.33; tive 0; Mismatches 0; Indels 0
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                                                                                                            Quint W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quint W,
                                                                                                            Haesebrouck F,
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                                                                                                                                                                                                                                                                                       Claim 2; Page 22-23; 132pp; English.
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                       99EP-00870035.
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                                                                                                            Ducatelle R, De Groote D,
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nes 20; Conserv
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                       25-FEB-1999;
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15-JAN-2001
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                                       Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
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Helicobacter 16SrRna DNA seguence R6XA001.
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                                                                 chronic gastritis; zoonoses; ss.
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                                                                                                            Candidatus Helicobacter bovis.
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(first entry)
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Matches 20; Conserv
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AAV66849;
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                                 This sequence represents a Helicobacter 16SrRNA sequence of the invention. A probe which specifically hybridises to the 16SrRNA sequence and a primer which specifically amplifies it are used for detecting and/or typing Helicobacter strains present in a biological sample (obtained from mammals preferably cattle and pigs) by hybridising or specifically amplifying the 16S rRNA gene target region of Helicobacter strains present in the biological sample with the primer or probe respectively. The 16S rRNA sequence is also used as a medicament. The 16S rRNA sequence is also used as a medicament. The 16S Helicobacter strains which cause gastric ulcers and chronic gastritis in mammals, particularly cattle and pigs. The method is also useful for detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
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Helicobacter strains which cause gastric ulcers and chronic gastritis in mammals, particularly cattle and pigs. The method is also useful for detection of zoonoses in humans. (Updated on 15-SBP-2003 to standardise OS field)
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100.0%; Score 20; DB 3; Length 1335;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                          Sequence 1335 BP; 364 A; 294 C; 393 G; 284 T; 0 U; 0 Other;
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(first entry)
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20; Conserv
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06-JAN-1999
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28-MAR-1997;

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                                                                                                                                       The present sequence represents a gene coding Chlamydia 16s ribosome RNA from Chlamydia psittaci. Also described in the present invention are: (1) a recombinant vector containing the above gene; and (2) a transformant transformed by the above recombinant vector. The nucleic acid, and primers which can hybridise to it, are used for the specific nucleic acid amplification detection of a Chlamydia genus microbe i.e. detection of PCR products. (Updated on 17-OCT-2003 to standardise OS field)
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                                    Chlamydia species ribosome genes, and primers derived from it - used for the nucleic acid amplification detection of Chlamydia species.
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                                                                                                                                                                                                                                                                                                                 Sequence 1548 BP; 410 A; 328 C; 452 G; 358 T; 0 U; 0 Other;
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                                                                                                   Claim 1; Page 14-15; 18pp; Japanese.
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(TOKU ) TOKUYAMA SODA KK.
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WPI; 1998-587294/50
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Matches 20; Conserv
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06-JAN-1999
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                                                                                                                            Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 13-14; 18pp; Japanese.
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                                                                                   Chlamydia 16S ribosome RNA gene #2.
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Best Local Similarity 100.0
Matches 20, Conservative
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(TOKU ) TOKUYAMA SODA KK.
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(TOKU ) TOKUYAMA SODA KK.
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28-MAR-1997; 28-MAR-1997;

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AAV66848;

RESULT 10 AAV66848

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The present sequence represents a gene coding Chlamydia 16s ribosome RNA a from Chlamydia psittaci. Also described in the present invention are: (1) a recombinant vector containing the above gene; and (2) a transformant transformed by the above recombinant vector. The nucleic acid, and primers which can hybridise to it, are used for the specific nucleic acid amplification detection of a Chlamydia genus microbe i.e. detection of PCR products. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense, bacterial 16s ribosomal RNA, rRNA, bacterial infection, human, food grain supplement, livestock; poultry, therapeutic, ds.
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                                                                                                                                                                                                     Chlamydia species ribosome genes, and primers derived from it
the nucleic acid amplification detection of Chlamydia species.
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(first entry)
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(TOKU ) TOKUYAMA SODA KK.
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Best Local Similarity
Matches 20; Conserv
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                                   28-MAR-1997;
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24-OCT-2001
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(1) a recombinant vector containing the above gene; and (2) a transformed by the above recombinant vector. The nucleic acid, and primers which can hybridise to it, are used for the specific nucleic acid amplification detection of a Chlamydia genus microbe i.e. detection of PCR products

    used for

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                       GGAGGAAGGCGAGGATGACG 1197
                                                                                                                                                                                                                                          Chlamydia 16S ribosome RNA gene #6
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GGAGGAAGGCGAGGATGACG 20
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Best Local Similarity 100.0
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(TOKU ) TOKUYAMA SODA KK.
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06-JAN-1999

AAV66850

AAS11021-AAS11034 represent the coding sequences of bacterial 16s ribosomal RNA (rRNA) genes. The sequences were used to design anti-

Disclosure, Page, 62pp, English.

Chlamydophila caviae

17-OCT-2003 06-JAN-1999

AAV66847;

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bacterial compounds comprising substantially uncharged antisense cligomers containing 8-40 nucleotide subunits, including a targeting nucleic acid sequence at least 10 nucleotides in length which is complementary to a bacterial 165 or 235 rRNA nucleic acid sequence. The antisense oligomers are used for treating a bacterial infection in a human or a mammalian singly produced by Escherichia coil, Salmonella typhimurium, Pseudomonas aeruginosa, Vibrio cholera, Neisseria gonorrhoea, Helicobacter pylori, Bartonella henselae, Haemophilus influenza, Shigalla dysenterae, Staphylococcus aureus, Mycobacterium tuberculosis, Streptococcus pneumoniae, Treponema palladium and Chamydia trachomatis. The antibacterial compound may be used as a food grain supplement in livestock and poultry food composition. Note: The present sequence is not shown in the specification but has been accessed from GenBank using the appropriate accession number given in the specification. (Updated on 06-NUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a gene coding Chlamydia 16s ribosome RNA from Chlamydia trachomatis. Also described in the present invention are: (1) a recombinant vector containing the above gene; and (2) a transformant transformed by the above recombinant vector. The nucleic acid, and primers which can hybridise to it, are used for the specific nucleic acid amplification detection of a Chlamydia genus microbe i.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia species ribosome genes, and primers derived from it - used for the nucleic acid amplification detection of Chlamydia species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 5; Length 1548; 100.0%; Pred. No. 0.33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia 16S ribosome RNA gene #7.
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(TOKU ) TOKUYAMA SODA KK.
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Query Match
100.0%; Score 20; DB 2; Length 1549;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0

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A190336 RC-BT029-
A1903431 RC-BT029-
BT742715 KX340029-
BT742715 KX340029-
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BF810332 RC-ET029-
BF81033 RC-ET029-
BF81030 RC-ET029-
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BC981048 RC-CT000
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BC9756 ME1-0016T
BF810198 RC-CT000
BC9756 ME1-0016T
BF810198 RC-CT000
BC9756 ME1-0016T
BF810198 RC-CT000
BC9756 RE-CO1000
BC9756 RE-CC-CT000
BC9756 RE-CC-CT000
BC9756 RC-CT000
BC9757 RC-CT000
BC97
AW947763 RC0-MT000
CD164995 ML1-0093T
H74424 126 Standar
AT000468 AT000468
BH831104 BACP92-L
CF33898 RCL1--03-
BX000722 BX000722
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1 (bases 1 to 122)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI903353 122 bp mRNA linear EST 30-MAR-2000
RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence.
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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CF199424 EST1023 T
CD088408 MC1-0050T
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                                                                                                                                August 4, 2004, 05:41:25; Search time 1393.25 Seconds (without alignments) 428.668 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                             55026578
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Matches 20; Conservative
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                                Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=RC&t2=RC-BT029-113_1.html&t3=100199&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev stage="Adult"
/clone_lib="BT029"
/note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2:
Smal; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Fax: +55-11-2700001
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PM3-BT0654-030300-002-d12 BT0654 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/mol type="mRNA"
/db_xref="taxon:9606"
/sex="female"
                                                                                                                                                                                                                                                                            Seq primer: puc 18 forward.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
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Best Local
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VERSION
KEYWORDS
SOURCE
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BE084285
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                                                                                                                                                                                                                                                                                                                        FEATURES
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/mol type="mkNa" | months | mol type="mkNa" | min-library was made by cloning products derived from Oregrass PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mkNa and cDNA amplification were performed under low stringency conditions."
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1 (bases 1 to 169)
Wang, Y., Yang, C., Jiang, J., Liu, G., Wu, J. and Liu, Z.
EST aquired from cDNA library of Tamarix androssowii treated with NaHCO3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST1023 Tamarix androssowii leaf Tamarix androssowii cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Northeast Forestry University
Hexing 26, Harbin, Heilongjiang, 150040, P.R. China
Tel: 086-451-219060.
Email: WANGYUCHENG1029@YAHOO.COM.CN.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="tracon:189785"
/tissue type="leaf"
/clone_lib="Tamarix androssowii leaf"

    168
    ramarix androssowii"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yucheng Wang
Forestry Source and Environment College
organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 bp
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Eukaryotes, Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases I to 205)

1 (bases I to 205)

1 (bases I to 205)

2 (bases I to 205)

2 (bases I to 205)

3 (bases I to 205)

3 (bases I to 205)

4 (bases I to 205)

5 (bases I to 205)

6 (b
                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCO-MT0006-110
300-021-d10&t3=2000-03-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence start: 20
High quality sequence stop: 186.
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ML1-0093T-D139-B11-U.G ML1-0093 Schistosoma mansoni cDNA clone
ML1-0093T-D139-B11.G, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone lib="MT0006"
/note="Corgan: marrow; Vector: puc18; Site_l: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA, and cDNA amplification were performed under low
                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Shotgun sequencing of the human transcriptome with ORF expressed
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                                        sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Departamento de Bioquimica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genet. 35 (2), 148-157 (2003)
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CD164995.1 GI:34701658
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Schistosoma mansoni
                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
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Matches 20; Conserv
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CD164995
LOCUS
DEFINITION
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SOURCE
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                                                                                                                             Sciiscosoma mainsoun.

Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Striggeidida; Schistosomatoidea; Schistosomatidae; Stristosoma.

Striggeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

I. (bases 1 to 174)

Syrigovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M., Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr., Kitajima,J.P., Adamson,R.E., Ashron,P.D., Bonaldo,M.F., Culson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho.P.L., Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A., Nascimento,A.L.T.O., Ohlweller,F.P., Reis,E.M., Ribeiro,M.A., Sak,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T., Rodriques,V., Madeira,A.M.B.M., Wilson,R.A., Menck,C.F.M., Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.

Transcriptome analysis of the accelomate human parasite Schistosoma
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Homo sapiens
Homo sapiens
Homo sapiens

Bukaryota; Metazaa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazaa; Chordata; Catarrhini; Hominidae; Homo.

Lobaes 1 to 186)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Magai, M.A., da Silva, W., Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-3091-2173

Fax: +55-11-3091-2186

Genome Project was derived from the FAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL http://bioinfo.iq.usp.br/schisto/
Flate: MCI-0050F-R112 row: 3 column: C.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/dlone="MC1-0050T-R112-C03.G"
/sex="mixed_pool"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="cercaria"
/lab_host="Biomphalaria glabrata"
/clone_lib="MC1-0050"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pGEM T-easy"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nat. Genet. 35 (2), 148-157 (2003)
22879926
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EST.
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Best Local Similarity 100.0%;
Matches 20; Conservative C
                                                                                                              Schistosoma mansoni
                                                                                 Schistosoma mansoni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 31-OCT-1995
                                                                      Fax: +55-11-3031-2186
Email: verjo@q.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassica napus
Watzyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
1 (bases 1 to 214)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. coli DH5a"
/clone lib="Standard"
/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; ESTS
were generated from the root cDNA library of Brassica
napus. The cDNA was synthesized from root poly(A) RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Nam, HG
Contact: Nam, HG
Plant Molecular Genetics Laboratory
Pohang University of Science and Technology
Dept. of Life Science, San31 Hyojadong, Pohang Kyungbuk 790-784,
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
Brasil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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126 Standard Brassica napus cDNA clone R185F, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 2
0.082;
hes 0; Indels
                                                                                                                                                                                                                                                /organism="Schistosoma mansoni"
                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:6183"
/clone="ML1-0093T-D139-B11.G"
                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pGEM T-easy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%; Score 20; Similarity 100.0%; Pred. No. 120; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                        /sex="mixed pool"
/dev_stage="miracidium"
/clone_lib="ML1-0093"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 825622792199
Email: nam@vision.postech.ac.kr
Seg primer: M13 forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="L. cv Naehan"
/db_xref="taxon:3708"
/clone="R185F"
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                                                            Tel: +55-11-3091-2173
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H74424
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AT000468 Brassica rapa guard cell Brassica rapa subsp. pekinensis
CDNA clone DGT85, mRNA sequence.
AT000468
BST.
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (Bases II to 221)
1 (Bases II to 221)
Bvaluation of 515 expressed sequence tags obtained from guard cells of Brassica campestris
Planta 202 (I), 9-17 (1997)
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Department of Life Science, Plant Molecular Genetics Laboratory
Department of Life Science and Technology
Pohang University of Science and Technology
San 31 Hyojadong, Pohang Kyungbuk 790-784, Korea
Email: hgm@bric.postech.ac.kr
Submitted through BRIC(Biological Research Information Center) of
Korea URL: http://bric.postech.ac.kr/.
Location/Qualifiers
     as
with Pharmacia's cDNA synthesis kit using oligo(dT) a primer. The Eco RI/Not I adaptor was ligated to the dSDNA. The cDNAs inserts were cloned into the pUC19 vector digested with EcoRI."
                                                                                                                                                                                                             Gaps
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Pristionchus pacificus
Eukarycta, Metazoa, Nematoda, Chromadorea, Diplogasterida,
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0
                                                                                                                       100.0%; Score 20; DB 14; Length 214;
ilarity 100.0%; Pred. No. 0.083;
Conservative 0; Mismatcher

    .221
    /organism="Brassica rapa subsp. pekinensis"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="guard_cell_protoplast"
/clone_lib="Brassica_rapa_guard_cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%; Score 20; DB 9; Similarity 100.0%; Pred. No. 0.083; 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/sub_species="pekinensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:51351"
/clone="DGT85"
                                                                                                                                                                                                                                                                                              124 GCAAACAGGATTAGATACCC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 GCAAACAGGATTAGATACCC 100
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/tissue_type="xylem"
/clone_lib="Pinus pinaster xylem"
/clone_lib="Compression wood was induced in four 14-year old maritime pine clones by artifitial bending. Control clone (in bending) were sampled for xylem associated with early wood and late wood at the beginning (April) and at the end (August) of the growing seasons. Differentiating xylem corresponding to Early wood, late wood, compression wood the cDNA-APIPP assay."
                                                                                                                                                                                                                                                                                                                                              BX000722 275 bp mRNA linear EST 03-DEC-2002 BX000722 Pinus pinaster xylem Pinus pinaster cDNA clone PPEM56, mRNA sequence.
BX000722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 bp mRNA linear EST 30-MAY-2001 CMO-BN0075-220200-237-h05 BN0075 Homo sapiens cDNA, mRNA sequence. BG874702 BG874702.1 GI:14251633 BST.
end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pinus pinaster
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophy
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pin
(Dases 1 to 275)
Le Provost, G., Paiva, J., Pot, D., Brach, J. and Plomion, P. Seasonal variation in transcript accumulation in wood forming tissue of maritime pine (Pinus pinaster Ait.) with emphasis on uppublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                     Length 248;
                                                                                                                                                 0; Indels
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Email: Frigerio@pierroton.inra.fr.
Location/Qualifiers
                                                                                                     Score 20; DB 14;
Pred. No. 0.084;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="PPEM56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Frigerio JM
Genetique et Amelioration 69
                                         regenerated media'
                                                                                     100.0%; SCU
100.0%; Pre
                                                                                                                                                                                                                                        159 GCAAACAGGATTAGATACCC 178
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sapiens
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Dukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza,
1 (bases 1 to 248)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev stage="proliferated callus on 2N6 media for 30 days"/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
                1 (bases I to 243)
Srintvasan, U., Sinz, W., Lanz, C., Bránd, A., Nandakumar, R.,
Raddatz, G., Witte, H., Keller, H., Kipping, I., Pires da Silva, A.,
Jesse, T., Millare, J., de Both, M., Schuster, S.C. and Sommer, R.J.
A BAC-based genetic linkage map of the nematode Pristionchus
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                                                                                                                                                                                                                                                                                                                                                                                     /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="var. California"
/db xref="taxon:54126"
/clone_lib="Pristionchus pacificus BAC ends"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 28; Length 243; 100.0%; Pred. No. 0.084; ive 0; Mismatches 0; Indels
                                                                                                                                                                   Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Max-Planck-Institute for Developmental
Tel: 00497071601371
Fax: 00497071601498
Eaxl: ralf. sommer@tuebingen.mpg.de
Class: BAC ends.
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/mol_type="mRNA"
/cultivar="Nackdong"
  Neodiplogasteridae; Pristionchus.
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/clone="RCL1--03-G23"
/tissue_type="callus"
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Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                   rel: +55-11-2704922
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 297)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMO-BN0075-220 200-237-h05&t2=2000-02-22&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 17

High quality sequence stop: 297.
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1 (Dases 1 to 301)
Dias Neco,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., Costafin,S., Costaf,F.F.,
Ragai,M.A., Garvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., Geoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
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mRNA sequence.
                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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à a

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Fax: +55-11-2707001
Bmail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM3-BN0075-240
200-101-h05&t3=2000-02-24&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence start: 19
High quality sequence stop: 301.
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/db xref="texon:9606"
/db xref="texon:9606"
/db xref="texon:9606"
/db xref="texon:9606"
/clone lib="BMO1075"
/note="forgan: breast normal; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products Site_2: Smal; A mini-library was made by cloning products derived from RESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
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1 (bases I to 12)

1 (bases I to 12)

1 (bases I to 2)

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvahlo,A.F.; Matsukuma,A., Bardin,S., Costa,F.F., Matsukuma,A., Bardin,S., Costa,F.F., Goldwan,G.H., deolivaire,P.S., Brunstein,A., deolivaire,P.S., Brunstein,A., deolivaire,P.S., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Laboratory of Concer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                  Paulo-SP,
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RC-BT029-070199-018 BT029 Homo sapiens cDNA, mRNA sequence.
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                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=RC&t2=RC-BT029-018.html
&t3=070199&t4=1)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 312)
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1 (bases 3 to 312)
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Email: asimpson@ludwig.org.br
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Eug Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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RC-BT029-110199-165 BT029 Homo sapiens CDNA, mRNA sequence.
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Location/Qualifiers
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                                                          /clone lib="BT029"
/note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; Amin:-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gaps

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Query Match 100.0%; Score 20; DB 39; Length 20; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 20; Conservative 0; Mismatches 0; Indels

1 GCAAACAGGATTAGATACCC 20

; OTHER INFORMATION: synthetic amplification primer US-09-940-860-1

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Sequence 1, Application US/09620375

SEQUENCE 1, ACCOUNTY OF THE SEQUENCE OF INVENTION:
TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
TITLE OF INVENTION: CHRONIC FATIGUE SYNDROME AND RELATED DISORDERS
FILE REFERENCE: INSCI.009A

CURRENT APPLICATION NUMBER: US/09/620,375

CURRENT FILING DATE: 1999-04-02

PRIOR PILING DATE: 1999-04-02

PRIOR PILING DATE: 1999-04-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 25
                                                                                 RESULT 2
US-09-281-655-1
US-09-281-655-1
Sequence 1, Application US/09283655
GENERAL INFORMATION:
APPLICANT: VOjdani, A.
TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
TITLE OF INVENTION: HONOR: US/09/283,655
CURRENT FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PRESEQ for Windows Version 3.0
SEQ ID NO :
LENGTH: 25
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100.0%; Score 20; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
, OTHER INFORMATION: Synthetic oligonucleotide primer US-09-283-655-1
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1 GCAAACAGGATTAGATACCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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LENGTH: 50
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GENERAL INFORMATION:
APPLICANT: Weisburg, William G.
APPLICANT: Lane, David Milliam G.
APLICANT: Lane, David Milliam G.
TITLE OF INVENTION: A METHOD FOR DETECTING AND IDENTIFYING
TITLE OF INVENTION: PATHOGENIC ORGANISMS USING TARGET SEQUENCES AS DETECTORS
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                                                                    APPLICANT: Vojdani, A.
TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
TITLE OF INVENTION: CHECONIC PATIGUE SYNDROME AND RELATED DISORDERS
FILE REPERENCE: IMSCI.009A
CURRENT APPLICATION NUMBER: US/10/715,220
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US/09/283,655
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRSTSEQ for Windows Version 3.0
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100.0%; Score 20; DB 39; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09940860;
GENERAL INFORMATION:
APPLICANT: Rochman, Richard
APPLICANT: Rochman, Richard
APPLICANT: Rochman, Richard
APPLICANT: Manjmudar, MOLECULAR DIAGNOSIS OF BACTEREMIA;
FILE REPERENCE: 01107.00185;
CURRENT APPLICATION NUMBER: US/09/940,860
CURRENT FILING DATE: 2001-08-29
PRIOR PPLIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 30
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic oligonucleotide primer US-10-715-220-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: synthetic amplification primer US-09-940-860-6
                   Sequence 1, Application US/10715220 GENERAL INFORMATION:
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APPLICANT: Hancer, Neil
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda B.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFRENCE: DAVILL39.002APC
CURRENT APPLICATION NUMBER: U5/10/343,319
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/AU01/00933
PRIOR APPLICATION NUMBER: AU PQ9090/2000
PRIOR FILING DATE: 2000-07-28
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ZIP: 02173

ZIP: 02173

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,935
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Pred. No. 0.14;
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100.0%; Score 20; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches
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contains in INFORMATION: Helicobacter pyloxi also. US-10-343-319-76
                                                                                                                                 NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA probe
                                                                                                                                                                                                                                                                                                                                                                                                               : 47 base pairs
nucleic acid
EDNESS: single
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                                                                                                         APPLICANT: Jacques, Nicholas A.
APPLICANT: Marcin, Fjelda E.
APPLICANT: Marcin, Fjelda E.
APPLICANT: Marcin, Fjelda E.
APPLICANT: Nardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139:002APC
CURRENT PELLING DATE: 2003-09-17
PRIOR ELLING DATE: 2001-09-17
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
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APPLICANT: Huncer, Neil
APPLICANT: Hancer, Nicholas A.
APPLICANT: Markin, Fjelda E.
APPLICANT: Markin, Fjelda E.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS:
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS:
TILE REFERENCE: DAVI139.002APC
CURRENT FILING DATE: 2003-09-17
CURRENT FILING DATE: 2003-09-17
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: PCT/AU01/00933
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SEQ ID NOS 106
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has 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA; ORGANISM: Thiomicrospira denitrificans US-10-343-319-80
                                     Sequence 80, Application US/10343319 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-343-319-81; Sequence 81, Application US/10343319; GENERAL INFORMATION:
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; ORGANISM: Neisseria meningitidis
US-10-343-319-81
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APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda E.
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Matches 20, Conservative
                                                                                    APPLICANT: Hunter, Neil
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                  US-10-343-319-80
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                                                                                                                                                                                                                                                           APPLICANT: Hunter, Neil
APPLICANT: Hunter, Neil
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fielda B.
APPLICANT: Martin, Fielda B.
APPLICANT: Martin, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICRORGANISMS
FILE REFERENCE: DAVIJ39,002APC
CURRENT APPLICATION NUMBER: US/11/343,319
CURRENT FILING DATE: 2003-09-17
PRICR FILING DATE: 2001-07-27
PRICR FILING DATE: 2001-07-27
PRICR PLINIG DATE: 2000-07-28
SPRICR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HUREL' Neil
APPLICANT: Uacques, Nicholas A.
APPLICANT: Uacques, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROCRGANISMS
FILE REFERENCE: DAVI139, OLOAPC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT APPLICATION NUMBER: PCT/AU01/00933
PRIOR APPLICATION NUMBER: PCT/AU01/00933
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SEQ ID NOS: 106
SEQ ID NO 79
LENGTH: 50
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0; Indels
0; Mismatches
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US-10-343-319-79
US-10-343-319-79
Sequence 79, Application US/10343319
GENERAL INFORMATION:
                                                                                                                                                                                                                   ; Sequence 77, Application US/10343319; GENERAL INFORMATION:
                                                                                 16 GCAAACAGGATTAGATACCC 35
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                                               1 GCAAACAGGATTAGATACCC 20
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CRGANISM: Treponema denticola
US-10-343-319-77
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; ORGANISM: Leptothrix mobilis
US-10-343-319-79
20; Conservative
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Best Local Simi]
Matches 20; (
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PRIOR APPLICATION NUMBER: AU PO9090/2000
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 84
LENGTH: 50
                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-343-319-84
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US-10-343-319-85
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APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/AU01/00933
PRIOR APPLICATION NUMBER: AU PQ9090/2000
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 83
LENGTH: 50
APPLICANT: Nardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REPERENCE: DAVI139.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
FILM APPLICATION NUMBER: PCT/A001/00933
PRIOR FILING DATE: 2001-09-17
PRIOR PILING DATE: 2001-07-27
PRIOR PILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Hunter, Neil
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda B.
APPLICANT: Nardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REPERANCE: DAVI139.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
PRIOR APPLICATION NUMBER: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/AU01/00933
PRIOR PILING DATE: 2001-07-27
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA; ORGANISM: Actinobacillus actinomycetemcomitans US-10-343-319-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 83, Application US/10343319; GENERAL INFORMATION: APPLICANT: Hunter, Neil
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; ORGANISM: Haemophilus influenzae
US-10-343-319-83
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LENGTH: 50
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OTHER INFORMATION: Also Vibrio cholerae, Pseudomonas aeruginosa, and OTHER INFORMATION: Rhodospirillum rubrum.
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                                                                                                                                                                                                                                                               Sequence 85, Application US/10343319
GENERAL INFORMATION:
APPLICANT: Hunter, Nicholas A.
APPLICANT: Hunter, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Nardkani, Mangala A.
ITILE OF INVENTION: A METHOD DO EFFECTING MICROORGANISMS
FILE REFERENCE: DAVI139.002APC
CURRENT PILLING DATE: 2003-09-17
PRIOR PILLING DATE: 2003-09-17
PRIOR PILLING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 85
LEYER: DNA
CURRANTS Salmonella typhi
                                                     Indels
Query Match 100.0%; Score 20; DB 49; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 20; Conservative 0; Mismatches 0;
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Job time : 1826.78 secs
                                                                                                      1 GCAAACAGGATTAGATACCC 20
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11111111 8448210088465	2000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ᲓᲝᲝᲓᲝᲝᲥᲥᲥᲥᲥᲥ ᲥᲡ७८८००। ८८५५	RESULT 1 AV295422 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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BG380134/c
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ORGANISM
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TITLE
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                                                                                                                     TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HG102240 410 bp mRNA linear EST 30-JAN-2001
RHIZ2_23_H01.b1_A003 Rhizome2 (RHIZ2) Sorghum propinguum cDNA, mRNA
seguence.
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/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="DH10B"
/clone lib="RikEN full-length enriched, 8 days embryo"
/clone lib="RikEN full-length enriched, 8 days embryo"
/note="Site l: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
GAGAGAAGGAACCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M. Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Cramaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Ozawa, Y., Muramatsu, M., Automated filtration-based high-throughput plasmid preparation system. Genome Rss. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Sorghum propinguum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                     Email: genome-resegec_riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa.M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
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Pred. No. 1e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="5730434H04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/strain="C57BL/6J"
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BG102240.1 GI:12617185
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100.0%;
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                                                                                                         Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Best Local Similarity 100.
Matches 18; Conservative
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BG102240/c
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Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9556
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sorghum propinguum"
/mol type="mRNA"
/db_xref="taxon:132711"
/clone lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site_1: Khoi, Site_2: EcoRi; The library was made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                        Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Far: 706 542 1860
                                                                                                                                                       Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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An EST database from Sorghum: Sorghum propinguum rhizomes
Unpublished (2000)
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
Seq primer: JEN REV
High quality sequence stop: 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Best Local Similarity
Marches 18; Conserv
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117 GGAGGAAGGCGAGGATGA 134
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Saccharum officinarum
                                                                                                 Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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CG093863/c
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CA199884/c
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                                                                                                                                                                      /db xref="taxon:10116"
/clone="UI-R-CS0-btp-d-11-0-UI"
/dev stage="ADULT"
/dev stage="ADULT"
/lab_host="BH10B (Life Technologies)"
/clone lib="UI-R-CS0"
/clone lib="UI-R-CS0"
/clone lib="UI-R-CS0"
/note="Weetor: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CS0
library is a normalized library constructed from the
following rat heart tissues: embryonic day 17, embryonic
day 19; embryonic day 21, adult day 1, adult day 12, adult
day 75, adult day 200. For a detailed description of the
library from which this clone was derived, please visit
our web site at ratest: eng.uiowa.edu. The subtraction has
been previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
TAG_TISSUE=rat heart pool
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PUFSX26TB ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTa0725F04,
CG093861
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Zea mays
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 530)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J., and
Bennetzen, J.
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Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 90.0%; Score 18; DB 12; Length 50 Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 18; Conservative 0; Mismatches 0; Indels
elements were found in this cDNA sequence: 1-23, >AT rich#Low complexity
Seq princh : M13 Forward
POLYATYES.
                                                                                                        1. .508
/organism="Rattus norvegicus"
                                                                                                                                       /mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
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Strain=B73"
/db xref="taxon:4577"
/clone="ZMMBTa0725F04"
                                                                               Location/Qualifiers
1. .508
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Class: sheared ends.
Location/Qualifiers
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TAG_SEQ=ATAAGATAAC"
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Unpublished (2003)
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Contact: Cathy Whitelaw
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CG093861
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CG093863.1 GI:33976157
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(Dases 1 to 567)
Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
/clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pcR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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/clone="zmxBFa0725F04"
/clone=lib="zm_06_1.0 KB"
/clone="Yector: pCR4-TOPO, Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
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9712 Medical Center Drive, Rockville, MD 20850, USA
9712 Medical Center Drive, Rockville, MD 20850, USA
9712 Medical Center Drive, Rockville, MD 20850, USA
Fax: 301-838-0208
Email: whitelaw@tigr.org
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                                                                                                                           90.0%; Score 18; DB 29; I 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0;
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/strain="B73"
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Class: sheared ends.
Location/Qualifiers
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Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFSXZ6TB
Contact: Cathy Whitelaw
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Query Match
Guery Match
Best Local Similarity luv..
Best Local 18; Conservative
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Zea mays
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CC657309/c
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/ Organism="Saccharum officinarum"
/mol_type="mRNA"
/db xref="taxon:4547"
/db xref="taxon:4547"
/clone="SCRIFL1013D09"
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/clone lib="FLH"
/note="Organ: Inflorescence at begining of development
/clone lib xrepared from polyA+ mRNA using SuperScript
Plasmid System Kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sixing between 0.8 and 1.5 KD were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                     Centrode Biologia Molecular e Engenharia Genetica
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1089
Email: partuda@unicamp.br
Clone distribution: Clone distribution information can be found
through the Brazilian Clone distribution Center (BCCC) at
http://www.bccenter.fcav.unesp.br
http://www.bccenter.fcav.unesp.br
plate: 013 row: D column: 09
Plate: 77 Promoter Primer.
Seg primer: 77 Promoter Primer.
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Saccharum officinarum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Saccharum.
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SCSBFL5014E09.g Saccharum officinarum FL5 Saccharum officinarum
cDNA clone SCSBFL5014E09 5', mRNA sequence.
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Contact: Arruda P Centro de Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas Caixa Postal 6010, 13083-970, Campinas SP, Brazil Fax: 55 19 3788 1089
                                                                                 1 (bases 1 to 573)
Vettore, A. L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
Genet. Moll. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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| Corganism="Casccharum officinarum" |
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| Clone | SCSBFL5014809" |
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OGJAO16TV ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMa0295D07,
genomic survey sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
ade; Panicoideae; Andropogoneae; Zea.
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Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br Plate: 014 row: E column: 09 Seq primer: 77 Promocher Primer. Location/Qualifiers
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methylation filtered genomic DNA library"
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Tel: 301-838-5843
Fax: 301-838-0208
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CC657309.1 GI:32060634
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VERSION KEYWORDS SOURCE ORGANISM

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RESULT 9 CG734728/c DEFINITION

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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM755 row: & column: 21

High quality sequence stop: 771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="adenocarcinoma cell line"
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/lab_host="DH10B (phage-resistant)"
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/note="Organ: overy; Vector: pOTB7; Site_1: XhoI; Site_2:
cloned into EconI/XhoI sites using the following s'
adaptor: GGCAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae, PACCAD clade; Panicoldeae; Andropogoneae; Zea.

(Dases 1 to 867)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Maize Genomics-Consortium

Unpublished (2003)

Other GSSS: PUTKEG4TB
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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Zea mays subsp. mays

Eukaryota; Viridiplante; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplante; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Lillopsida; Poales; Poacea; PACCAD

alade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 784)

S Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.

S Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.

S Yu,Y., Ming,R.

Sequencing of the maize genome

Unpublished (2003)

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

Fax: 520 621 9288

Email: http://genome.arizona.edu
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BE743778 BE743770
EST 15-SEP-2000
                                                                                                                                                                                                                                                                                     July 28 22-0CT-2003 2MMBBb0290C20.f ZMMBBb Zea mays subsp. mays genomic clone ZMMBBb0290C20 5', genomic survey sequence.
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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Plate: 0290 row: C column: 20
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
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FEATURES

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CG038933 972 bp DNA linear GSS 19-AUG-2003 PUFLB28TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0674F0B, genomic survey sequence. CG038933.1 GI:33911089
951 bp DNA linear GSS 19-AUG-2003 purings MNB Inear GSS 19-AUG-2003 genomic survey sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 972)
1 (bases 1 to 972)
Resnick, A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida, Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 951)
Whitelaw, C.A., Ouackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
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COT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR Medical Center Drive, Rockville, MD 20850, USA 9712 Medical Center Drive, Rockville, MD 20850, USA Fax: 301-838-0208
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ilarity 100.0%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 0;
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Unpublished (2003)
Other_GSSs: PUFLB28TD
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Unpublished (2003)
Other GSSs: PUFLB28TB
Contact: Cathy Whitelaw
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                                                                                                                         CG038934.1 GI:33911090
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Class: sheared ends.
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Fax: 301-838-0208
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CG038933
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CoT selected genomic DNA libzary"
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Mhitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, J. Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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/organism="Zea mays"
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Class: sheared ends.
Location/Qualifiers
                                             Class: sheared ends.
Location/Qualifiers
1. .867
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Unpublished (2003)
Other GSSs: PUFDX67TB
Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: whitelaw@tigr.org
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Fax: 301-838-0208
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Best Local
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BZ803618/c
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TITLE JOURNAL COMMENT

FEATURES

ORIGIN

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Indels

Email: whitelaw@tigr.org

RESULT 13 CG038934/c

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Length 951;

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Zea mays
Zea mays
Sea mays
Sea mays
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
( hosses i to 992)
Resnick, A., Fraser, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
AL Unpublished (2003)
Other GSSS: PUFDX67TD
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BZ803611 GI:29012211 992 bp DNA linear GSS 17-MAR-2003 PUFDX67TB ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa297K14, genomic survey sequence.
BZ803611.1 GI:29012211
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                                                        1. .972

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CoT selected genomic DNA library"
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90.0%; Score 18; DB 28; Length 992;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                Query Match 90.0%; Score 18; DB 29; Length 97 Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 18; Conservative 0; Mismatches 0; Indels
Seg primer: TR
Class: sheared ends.
Location/Qualifiers
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BZ803611
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1 GGAGGAAGGCGAGGATGA 18

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Job time : 1397.25 secs

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NAME/KEY: misc_feature
; LOCATION: 363
; OTHER INFORMATION: s=g or c
US-10-793-479-14013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: modified_base
LOCATION: (494)
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ORGANISM: Homo sapiens
                                                                                                                                                       US-10-793-479-14013
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3171, Application US/10417884A
Sequence 3171, Application US/10417884A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A DOUGETE-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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100.0%; Score 20; DB 7; Length 279;
Bewt Local Similarity 100.0%; Pred. No. 0.021;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                       100.0%; Score 20; DB 7; Length 279; liarity 100.0%; Pred. No. 0.021; Conservative 0; Mismatches 0; Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/417,884A
FILING DATE: 17-Apr-2003
PRIOR APPLICATION NUMBER: US/09/107,532
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                 ), NAME/KEY: misc_feature
), LOCATION: (B) LÖCATION 1...279
), SEQUENCE DESCRIPTION: SEQ ID NO: 3170:
US-10-417-884A-3170
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LOCATION: (B) LOCATION 1...279
SEQUENCE DESCRIPTION: SEQ ID NO: 3171:
US-10-417-884A-3171
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REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEO ID NO: 3171:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
ORGANISM: Enterococcus faecium
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COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER.READABLE FORM:
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                                                                                                                                                            Query Match
Best Local Similarity
Matches 20; Conservat
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APPLICANT: PERMODET, JEAN-LUC
APPLICANT: GUERINERAL MICHEL
APPLICANT: GINGERINERAL MICHEL
APPLICANT: GINGERINERAL
ATTLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
TITLE OF INVENTION TOWNER: FR9915032
PRIOR FILING DATE: 2000-01-29
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE PATENTIN Ver. 3.2
LENGTH: 1113
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US-10-486-307-5/c
US-10-486-307-5/c
Sequence 5, Application US/10486-307
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: GENERS ENCODING BAEYER-VILLIGER MONOCXYGENASES
TITLE OF INVENTION: 2004-02-05
CURRENT PILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: 60/315,546
FRIOR APPLICATION NUMBER: 60/315,546
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Microsoft Office 97
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100.0%; Score 20; DB 8; Length 1113;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0
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Pred. No. 0.019;
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100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 20; Conservative 0; Mismatches
     0; Mismatches
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APPLICANT: JEANNIN, PASCALE
                                                                                                            696 GCAAACAGGATTAGATACCC 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; ORGANISM: Brachymonas sp. CHX
US-10-486-307-5
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ORGANISM: Unknown organism
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-148-328B-70
     20;
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     Matches
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GENERAL INFORMATION:
APPLICANT: Rosenberg, Eugene
APPLICANT: Ros, Eliora Z.
APPLICANT: Ror, Eliora Z.
APPLICANT: Ror, Eliora Z.
APPLICANT: Ror, Eliora Z.
APPLICANT: ACID MAY
TITLE OF INVENTION: BIOREMEDIATION OF PETROLEUM POLLUTION USING WATER-INSOLUBLE URIC
FILE REPERENCE: 27821
CURRENT APPLICATION NUMBER: PCT/IL04/00351
CURRENT PILING DATE: 2004-04-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PERNODET, JEAN-LUC
APPLICANT: PERNODET, JEAN-LUC
APPLICANT: GERNINGY, MICHEL
APPLICANT: GIRGINEAU, MICHEL
APPLICANT: GIRGINEAU, MICHEL
APPLICANT: GIRGINEAU, MICHEL
APPLICANT: GIRONET, PASCAL
TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: OF NOVEL COMPOUNDS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
FILE REFERENCE: 03806.0547-00000
CURRENT APPLICATION NUMBER: US/10/148,328B
CURRENT APPLICATION NUMBER: ER9915032
PRIOR APPLICATION NUMBER: PET/FR00/03311
PRIOR FILING DATE: 2000-11-29
PRIOR PELING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/209,800
PRIOR APPLICATION NUMBER: 60/209,800
PRIOR APPLICATION NUMBER: 60/209,800
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PARCHILIN VOY: 3.2
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                                                                            Query Match 100.0%; Score 20; DB 8; Length 600; Best Local Similarity 100.0%; Pred. No. 0.02; Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Origin of the sequence: soil organism US-10-148-328B-75
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Pred. No. 0.019;
; OTHER INFORMATION: variable nucleotide US-10-148-328B-74
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GENERAL INFORMATION:
                                                                                                                                                                                                                           265 GCAAACAGGATTAGATACCC 284
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Best Local Similarity
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SEQ ID NO 5
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616 GCAAACAGGATTAGATACCC 635
1 GCAAACAGGATTAGATACCC 20
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ORGANISM: Unknown organism
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Matches 20; Conservative
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                  Sequence 100, Application US/10148328B

Sequence 1010, Application US/10148328B

GENERAL INFORMATION:
APPLICANT: DEANNIN, PASCALE
APPLICANT: DEANNIN, PASCALE
APPLICANT: GUBRINEAU, MICHEL
APPLICANT: GUBRINEAU, MICHEL
TITLE OF INVENTION: MARCHEL
TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
TITLE OF INVENTION: MUMBER: EX915030
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 1999-11-29
PRIOR PELICATION NUMBER: PCT/FR00/03311
PRIOR APPLICATION NUMBER: PCT/FR00/03311
PRIOR PELING DATE: 2000-06-07
PRIOR PELING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 100
LENGTH: 1197
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US-10-148-328B-81

i Sequence 11 Application US/10148328B

j GENERAL INFORMATION:
APPLICANT: JEANNIN, PASCALE
APPLICANT: JEANNIN, PASCALE
TITLE OF INVENTION: MUCHEL
APPLICANT: SIMONET, PASCAL
TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
CURRENT APPLICATION NUMBER: US/10/148,328B
CURRENT FILING DATE: 1099-11-29
PRIOR FILING DATE: 1099-11-27
PRIOR PELLING DATE: 2000-01-27
PRIOR PELLING DATE: 2000-01-27
PRIOR PELLING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PALENTIN VET. 3.2
SEQ ID NO 81
LENGTH: 1210
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Best Local Similarity 100.0%; Score 20; DB 8; Length 1210;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels (
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ORGANISM: Unknown organism
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ORGANISM: Unknown organism
   RESULT 9
US-10-148-328B-100
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US-10-148-328B-71

US-10-148-328B-71

US-10-148-328B-71

Sequence 71, Application US/10148328B

GENERAL INFORMATION:
APPLICANT: JEANNIN, PRASCALE
APPLICANT: GUERINEAU, MICHEL
APPLICANT: SIMONET, PASCALE
APPLICANTON: MATHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: AMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: AMPLER: 2002-05-29
CURRENT APPLICATION NUMBER: PC7/FN00/03311
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-06-07
SEQ ID NO 71
LENGTH: 1228
TWOST. NAN.
SEQ ID NO 71
LENGTH: 1228
RESULT 11
US-10-148-326B-66

; Sequence 66, Application US/10148328B
; Geruence 66, Application US/10148328B
; Geruence 66, Application US/10148328B
; Geruence 66, Application US/1014832BB
; Geruence 66, Application US/1014832BB
; GERNEAL INFORMATION: PASCALE
; APPLICANT: PERROBET, DEAN-LUC
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: BATHOD FOR CETAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS FROM AN ENVIRONMENT;
; TITLE OF INVENTION: CONFOCUDE
; TITLE OF INVENTION: CONFOCUDE
; TITLE OF INVENTION: OF NOVEL COMPOUND
; TITLE OF INVENTION: CONFOCUDE
; TITLE OF INVENTION: CONFOCUDE
; TITLE OF INVENTION: CONFOCUDE
; TITLE OF INVENTION NUMBER: US/10/148,328B
; CURRENT FILING DATE: 2000-05-29
; PRIOR PELLING DATE: 1999-11-27
; PRIOR PELLING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: FC1/FR00/03311
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SEQ ID NO 66
; SEQ ID NO 66
; LENGTHARE: PALENTIN VEY. 3.2
; SEQ ID NO 66
; LENGTHARE: PALENTIN VEY. 3.2
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ORGANIZAM: Unknown organism
FEATURE:
OTHER INFORMATION: Origin of the sequence: soil organism
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PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 76
LENGTH: 1236
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US-10-148-328B-67
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GENERAL INFORMATION:
APPLICANT: JEANNIN, PASCALE
APPLICANT: PERNODET, JEAN-LUC
APPLICANT: GENENBAU, MICHEL
APPLICANT: GENENBAUG, MICHEL
APPLICANT: GENENBAUG, MICHEL
APPLICANTON: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: GENENGE, COMPOUNDS
FILE REFERENCE: 03806.0547-0000
FILE REFERENCE: 03806.0547-0000
CURRENT PELING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: FR9915032
FRIOR APPLICATION NUMBER: FC7/FR00/03311
FRIOR APPLICATION NUMBER: 60/209,800
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-37
FRIOR FILING DATE: 2000-13-37
FRIOR PARCE FILING DATE: 2000-13-37
FRIOR FILING DATE: 2000-13-37
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APPLICANT: DEMNNIN, PASCALE
APPLICANT: PERMODET, JEAN-LUC
APPLICANT: GURRILNEAU MICHEL
APPLICANT: SIMONET, PASCAL
TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: SEMULE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
TITLE APPLICATION UMBER: 12,10/148,328B
CURRENCE: 2002-05-29
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                                                                           Query Match
100.0%; Score 20; DB 8; Length 1225;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/209,800
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NAME/KEY: modified_base

LOCATION: (435)

OTHER INFORMATION: variable nucleotide
US-10-148-328B-98
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ORGANISM: Unknown organism
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-10-148-328B-98
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               US-10-148-328B-71
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BERNODET, JEAN-LUC
APPLICANT: GINERINBAD, MICHEL
APPLICANT: GINERINBAD, MICHEL
APPLICANT: GINERINBAD, MICHEL
APPLICANT: GINERINBAD, MICHEL
APPLICANT: GINERINBAD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: OF NOVEL COMPOUNDS
FILE REFERENCE: 03806.0547-00000
CURRENT APPLICATION NUMBER: US/10/148,328B
PRIOR APPLICATION NUMBER: PCT/FR00/03311
PRIOR PILING DATE: 1999-11-29
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-66-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PATCHLING OF 3.2
LENGHALL 1237
LENGHI: 1237
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100.0%; Score 20; DB 8; Length 1237;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                    Length 1236;
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                                                     FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-76
                                                                                                                                                              Query Match
100.0%; Score 20; DB 8;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 67, Application US/10148328B GENERAL INFORMATION:
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ORGANISM: Unknown organism
TYPE: DNA
ORGANISM: Unknown organism
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Second Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NOS: 369326
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US-10-425-115-29000

| Sequence 29000, Application US/10425115
| SEQUENCE 29000, Application US/10425115
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Cao, Yongwei
| APPLICANT: Cao, Yongwei
| TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TILLE OF INVENTION: Plants
| FILE REFERENCE: 38-21(53222)B
| CURRENT APPLICATION NUMBER: US/10/425,115
Sequence 70573, A Sequence 4335, A Sequence 125836, Sequence 125836, Sequence 126896, A Sequence 25387, A Sequence 25387, A Sequence 5, Appli Sequence 5, Appli Sequence 21759, A Sequence 21759, A Sequence 21759, A Sequence 21759, A Sequence 40086, A Sequence 40086, A Sequence 40086, A Sequence 40086, A
                                                                                                                                                                                                                             Sequence 21759, A. Sequence 21760, A. Sequence 40085, A. Sequence 103979, Sequence 133306, Sequence 99222, A. Sequence 13537, A. Sequence 13537, A.
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US-10-425-115-70573
US-10-767-701-22517
US-09-39-72064-4333
US-10-425-115-125836
US-10-425-115-198986
US-10-425-115-198986
US-10-425-115-198986
US-10-425-115-138986
US-10-363-345A-26387
US-10-620-246-5
US-10-620-246-5
US-10-620-345A-21759
US-10-363-345A-21759
US-10-363-345A-40085
US-10-363-345A-40085
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US-10-363-345A-40085
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US-10-425-115-133306
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100.0%; Pred. No. 0.71;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)...(850)
OTHER INFORMATION: unsure at all n locations
FEATURE:
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; Sequence 28998, Application US/10425115
; GENERAL INFORMATION:
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     Query Match
Best Local Similarity
Matches 18; Conserv
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ORGANISM: Zea mays
   77850
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NAME/KEY: unsure
     LENGTH:
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247.629 Million cell updates/sec
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                                                                                                                                 August 4, 2004, 06:43:54; Search time 199.036 Seconds
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1. /cgn2_6/ptodate/2/pna/USO6_NEW_COMB.seq:*

2. /cgn2_6/ptodate/2/pna/USO6_NEW_COMB.seq:*

3. /cgn2_6/ptodate/2/pna/USO7_NEW_COMB.seq:*

5. /cgn2_6/ptodate/2/pna/USO9_NEW_COMB.seq:*

5. /cgn2_6/ptodate/2/pna/USO9_NEW_COMB.seq:*

6. /cgn2_6/ptodate/2/pna/USO1_NEW_COMB.seq:*

7. /cgn2_6/ptodate/2/pna/USO1_NEW_COMB.seq:*

8. /cgn2_6/ptodate/2/pna/USO1_NEW_COMB.seq:*

9. /cgn2_6/ptodate/2/pna/USO0_NEW_COMB.seq:*

9. /cgn2_6/ptodate/2/pna/USO0_NEW_COMB.seq:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-425-115-109468
US-10-767-9704-14389
US-10-767-9704-14389
US-10-425-115-1150914
US-10-767-9704-28210
US-10-767-9704-28210
US-10-767-971-27370
US-10-425-115-122047
US-10-425-115-122047
US-10-21-17448-297
US-10-674-124A-38
US-60-582-609-23584
US-60-582-609-23584
US-10-767-701-30539
US-10-767-701-30539
US-10-430-201-4832-105-10-205-25
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                                                                                                                                                                                                                                                                                                                                          4754066 seqs, 1232178907 residues
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                                                                                             OM nucleic - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Match 1
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Perfect score:
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Best Local Similarity 100.
Matches 17; Conservative
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; SEQ ID NO 43
; LENGTH: 1073
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-473-974-43
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Best Local Similarity
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-767-701-14989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-425-115-109468/C
US-10-425-115-109468/C
Sequence 109468, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 109468
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Sequence 43, Application US/10473974

GENERAL INFORMATION:
APPLICANT: ROWAN ROMAN, SERGIO
APPLICANT: ROWAN ROLAND
APPLICANT: CALL, KATHERINE
APPLICANT: THEILHABER, JOACHIM
APPLICANT: AMANDA
APPLICANT: BUSHNELL, FIEVEN
APPLICANT: BUSHNELL, STEVEN
CURRENT FILING DATE: 2003-10-03
FRIOR FILING DATE: 2003-10-03
FRIOR APPLICATION NUMBER: BOYON APPLICANT APPLICATION NUMBER: BOYON APPLICANT APPLICATION NUMBER: BOYON APPLICANT APPLICANT APPLICATION NUMBER: BOYON APPLICANT APPLICANT APPLICATION NUMBER: BOYON APPLICANT APPLICANT APPLICANT APPLICATION NUMBER: BOYON APPLICANT APPLICANT APPLICATION NUMBER: BOYON APPLICANT AP
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US-10-425-115-29000
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US-10-425-115-109468
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            CURRENT FILING DATE: 2003-04
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 29000
LENGTH: 2551
                                                                                                                                                                       TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Zea mays
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US-10-15-15-151508

Sequence 151508, Application US/10425115
Sequence 151508, Application US/10425115
Sequence 151508, Thomas J.
Sequence 151508, Thomas J.
Sequence 151508. Thomas J.
Sequence 151508. Thomas J.
Septicant: Lacour, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: And Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Number US-153222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
EDENGTH: 2097
                                                                                                                                                                                                                                                                                                               Sequence 14989, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Application Mucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 14989
LENGTH: 1847
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Query Match 85.0%; Score 17; DB 7; Length 1073; Best Local Similarity 100.0%; Pred. No. 2.6; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS9317_1
US-10-767-701-14989
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US-10-425-115-151508
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LOCATION: (1)..(2097)
OTHER INFORMATION: unsure at all n locations
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Gaps

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5)222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 38956
LBNGTH: 551
TYPE: Number OF SEQ ID NOS: 369326
                     APPLICANT: Cao, Yorgwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Diants and Uses Thereof For Plant Improvement
FILE REPERENCE: 38-21(5335)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 28210
LENGTH: 510
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APPLICANT: LA ROSA, Thomas J.
APPLICANT: Excelic, David K.
APPLICANT: ACON, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERBUCE: 38-21(53222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
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100.0%; Pred. No. 9;
tive 0; Mismatches
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NAMB/KEY: unsure
LOCATION: (1)..(551)
CTHER INFORMATION: unsure at all n locations
FEATURE:
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GENERAL INFORMATION:
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US-10-767-701-28210
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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ses 16; Conserv
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ORGANISM: Zea mays
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Matches
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 130914
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Sequence 22770, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cabo, Yongweic
APPLICANT: Cabo, Yongweic
APPLICANT: APPLICANT: ADDITION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-2153535 B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 22770
LENGTH: 407
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8.9;
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US-10-425-115-130914
  Mismatches
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80.0%; Score 16;
Best Local Similarity 100.0%; Pred. No.
Matches 16; Conservative 0; Mismatcl
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100.0%; Pred. No.
:ive 0; Mismatc
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US-10-767-701-22770
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GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
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                                           2 GAGGAAGGCGAGGATGA
  Conservative
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ORGANISM: Sorghum bicolor
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Best Local Similarity
Matches 16; Conserv
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Best Local Similarity 100.
Terhes 16; Conservative
  16; Conservative
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    Matches
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Sequence 158496, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322.)
FILE REFERENCE: 38-21(5322.)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 158496
LENGTH: 1601
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18-10-426075, Application US/10425115
Sequence 126075, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Excalic, David K.
APPLICANT: Acai, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REPREMENCE: 38-21(5322)
TITLE OF INVENTION: Plants
FILE REPREMENCE: 163222)
CURRENT APPLICATION NUMBER: US/103223
CURRENT FILING DATE: 2003-04-28
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 126075
LENGTH: 788
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Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 16; Conservative 0; Mismatches 0; Indels
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9.1;
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US-10-425-115-158496
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, OTHER INFORMATION: Clone ID: MRT4577_42791C.1
US-10-425-115-122047
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US-10-425_115-126075
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80.0%; Score 16; DB
Best Local Similarity 100.0%; Pred. No. 9.1
Matches 16; Conservative 0; Mismatches
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    NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 122047
LENGTH: 677
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Best Local Similarity
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ORGANISM: Zea mays
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                                                                                TYPE: DNA
ORGANISM: Zea mays
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APPLICANT: TAMIYA, Gen
APPLICANT: TAMIYA, Gen
TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
FILE REPERENCE: ORIN-003CIP
CURRENT PAPLICATION NUMBER: US/10/674,124A
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 10/257,511
PRIOR APPLICATION NUMBER: PCT/JP00/07621
PRIOR APPLICATION NUMBER: D2000-0112699
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: JP2002-383869
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-01-209
NUMBER OF SEQ ID NOS: 27110
SEQ ID NO 38
LENGTH: 144
US-10-221-7148-297
Sequence 297, Application US/10221714B
GRNERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
TITLE OF INVENTION: tumor suppressor genes and oncogenes
TITLE OF INVENTION: tumor suppressor genes and oncogenes
TITLE OF INVENTION: tumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10013826.1
PRIOR APPLICATION NUMBER: DE 10013826.1
PRIOR APPLICATION NUMBER: DE 10013826.1
PRIOR PILING DATE: 2000-04-07
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100.0%; Pred. No. 9.5;
tive 0; Mismatches 0; Indels
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TYPE: DNA
CRANISM: Homo sapiens
CRANISM: Homo sapiens
CRANISM:
CREATURE:
COTHER INFORMATION: DISO7_10007639
FEATURE:
COTHER INFORMATION: Located on chromosome 1
COTHER INFORMATION: Chromosomal short arm and 5'-terminus of this base
COTHER INFORMATION: Sequence: 5692908
FEATURE:
COTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
COTHER INFORMATION: Sequence listing upward to telomere on chrosomal short arm and
COTHER INFORMATION: Sequence listing upward to telomere on chrosomal short arm and
COTHER INFORMATION: S'-terminus of this base sequence: 168636
US-10-674-124A-38
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75.0%; Score 15; DB 7; Length 144;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 0; Indels
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Search completed: August 4, 2004, 11:43:44 Job time: 200.036 secs

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Sequence 19, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 21, Appl
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Sequence 23, Appl
Sequence 728, Appl
Sequence 728, Appl
Sequence 450, Appl
Sequence 5, Appli
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; Publication No. US200400055531
; GENERAL INFORMATION:
APPLICANT: Rothman, Richard
; APPLICANT: Rothman, Richard
; APPLICANT: Rothman, Mulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00188:
CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT APPLICATION NUMBER: 60/229,376
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR APPLICATION STEEL SOUTO-08-31
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 1
; SEQ ID NO 1
LENGTH: 20
US-10-343-319-89

US 10-343-319-90

US 10-343-319-91

US 10-343-319-99

US 10-343-319-99

US 10-343-319-102

US 10-343-319-102

US 10-343-319-103

US 10-3410-340-105

US 10-410-040A-19

US 10-410-040A-16

US 10-410-040A-20

US 10-410-040A-21

US 10-213-878-5

US 10-213-878-5

US 10-20-37-297-2

US 10-20-37-297-2

US 10-10-213-878-5

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US 10-10-213-878-5

US 10-10-213-878-5
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 US-09-940-860-1
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                                                                                                      August 4, 2004, 07:44:29; Search time 180.964 Seconds (without alignments) 541.892 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, A
Sequence 76,
Sequence 77,
Sequence 79,
Sequence 80,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 82,
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Sequence 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Cgn2_6/ptodata/2/pubpna/US07_PUBCCMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                   6445838
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-715-220-1
US-10-343-319-76
US-10-343-319-77
US-10-343-319-77
US-10-343-319-81
US-10-343-319-81
US-10-343-319-83
US-10-343-319-83
US-10-343-319-85
US-10-343-319-85
US-10-343-319-85
US-10-343-319-85
US-10-343-319-85
US-10-343-319-85
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                                                                                                                                                                                                                                                                                   3222919 segs, 2451570024 residues
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                                                                           - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Gaps

Result No.

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APPLICANT: Vojdani, A.

TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
TITLE OF INVENTION: CHRONIC FAIIGUE SYNDROME AND RELATED DISORDERS
FILE REPERENCE: IMSCT. 1009A
CURRENT APPLICATION NUMBER: US/10/715,220
CURRENT APPLICATION NUMBER: US/9/283,655
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 8
SOFUTARE: FastSEQ for Windows Version 3.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08940860; Publication No. US2004000555A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GAPLICANT: Rothman Richard; APPLICANT: Rothman, Molecular DIAGNOSIS OF BACTEREMIA; FITUE OF INVENTION: WOMER: US/09/940,860; CURRENT APPLICATION NUMBER: US/09/940,860; CURRENT FILING DATE: 2001-08-29; PRIOR APPLICATION NUMBER: 60/229,376; PRIOR APPLICATION NUMBER: 60/229,376; PRIOR APPLICATION NUMBER: 60/229,376; PRIOR FILING DATE: 2000-08-31; NUMBER OF SEQ ID NOS: 7; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 6; IENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hunter, Neil
APPLICANT: Jacques, Nicholas A.
APPLICANT: Jacques, Nicholas A.
APPLICANT: Marchin, Filda E.
APPLICANT: Marchin, Filda E.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139.002ARC
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PST/AU01/00933
                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Synthetic oligonucleotide primer US-10-715-220-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: synthetic amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-343-319-76
, Sequence 76, Application US/10343319
; Publication No. US20040072242Al
, GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 20; DB 12; Length 50; Best Local Similarity 100.0%; Pred. No. 0.024; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 77, Application US/10343319
; Bequence 77, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Martin, Fjelda E.
; PILE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS; TILE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS; TILE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS; TILE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS; PRIOR FILING DATE: 2003-09-17
; PRIOR FILING DATE: 2000-07-27
; PRIOR FILING DATE: 2000-07-28
; NUMBER: OF SEQ ID NOS: 106
; SEQ ID NO 77
; ELNGTH: 50
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APPLICANT: Jacques, Nicholas A.
APPLICANT: Jacques, Nicholas A.
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda B.
APPLICANT: Martin, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICRORGANISMS
FILE REFERENCE: DAVILL39.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
PRIOR APPLICATION NUMBER: PCT/AU01/00933
PRIOR PILING DATE: 2001-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 12; 100.0%; Pred. No. 0.024;
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                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (0)...(0)
...OTHER INFORMATION: Helicobacter pylori also.
US-10-343-319-76
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: AU P09090/2000
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 76
LENGTH: 50
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Publication No. US20040072242A1
GENERAL INFORMATION:
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ORGANISM: Campylobacter jejuni
FEATURE:
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US-10-343-319-77
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105-10-343-319-82

Sequence 82, Application US/10343319

Sequence 82, Application US/10343319

Publication No. USCO04007224241

GENERAL INFORMATION:
APPLICANT: Hunter, Neil
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin Martin E.
APPLICANT: Martin Martin Martin E.
CURRENT APPLICATION NUMBER: US/10/343,319

CURRENT PILING DATE: 2003-09-17

PRIOR FILING DATE: 2001-07-27

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 106

SOUTHARE: PASTERE 2000-07-28

NUMBER OF SEQ ID NOS: 106

SEQ ID NO 82

LENGTH: 50
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                                                                                                                                                                             Length 50;
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APPLICANT: Hunter, Neil
APPLICANT: Hunter, Neil
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Mardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS:
FILE REPERENCE: DAVI19: 0.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2003-09-17
PRICR APPLICATION NUMBER: PCT/AU01/00933
PRICR APPLICATION NUMBER: AD P09090/2000
PRICR APPLICATION NUMBER: AD P09090/2000
PRICR APPLICATION NUMBER: AU P09090/2000
NUMBER OF SEQ ID NOS: 106
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                      Score 20; DB 12;
Pred. No. 0.024;
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       ; LENGTH: 50
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-343-319-81
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                                                                                                                                                                             100.0%;
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                                                                                                                                                 Query Match
Best Local Similarity 100.0
20; Conservative
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LENGTH: 50
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Sequence 80, Application US/10343319
Sequence 80, Application US/10343319
Publication No. US20040072242A1
GENERAL INFORMATION:
APPLICANT: Hunter, Neil
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda B.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139,002APC
CURRENT APPLICATION NUMBER: 2003-09-17
PRIOR PILING DATE: 2003-09-17
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 80
LENGTH: 50

"WANTER COMMENTION OF THE COMMENT OF THE
                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.024;
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APPLICANT: Hunter, Neil
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjeldaa A.
APPLICANT: Martin, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS;
FILE REFERENCE: DAVI139:003APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2003-09-17
PRIOR FILING DATE: 2001-07-27
PRIOR PLILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FasteEQ for Windows Version 4.0
SEQ ID NO 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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PRIOR APPLICATION NUMBER: AU PQ9090/2000
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SSCTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 79
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Thiomicrospira denitrificans
US-10-343-319-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 81, Application US/10343319
Publication No. US20040072242A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCAAACAGGATTAGATACCC 20
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                                                                                                                                                                                                      TYPE: DNA; CRGANISM: Leptothrix mobilis US-10-343-319-79
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Best Local Similarity 100.0
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jacques, Nicholas A.
APPLICANT: Jacques, Nicholas B.
APPLICANT: Martin, Fjelda B.
APPLICANT: Martin, Fjelda B.
APPLICANT: Nardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REPERENCE: DAVI139.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
FRICR PLING DATE: 2003-09-17
PRICR PLING DATE: 2001-07-27
PRICR APPLICATION NUMBER: PCT/AU01/00933
PRICR APPLICATION NUMBER: BCT/AU01/00933
PRICR APPLICATION NUMBER: AU PQ9090/2000
PRICR ETLING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SEQ ID NO SEQ ID NOS: 106
SEQ ID NO SO: 106
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SEQ ID NO SO: 106
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APPLICANT: Marchin, Fjelda E.
APPLICANT: Marchin, Fjelda E.
APPLICANT: Marchin, Fjelda E.
APPLICANT: Nardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS.
FILE REPERENCE: DAVI139.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2000-09-17
FRIOR APPLICATION NUMBER: PCT/AU01/00933
FRIOR FILING DATE: 2000-07-27
FRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SEQ.ID NOS: 106
SEQ.ID NO 88
LENGTH: 50
100.0%; Score 20; DB 12; Length ilarity 100.0%; Pred. No. 0.024; Conservative 0: Mismathle
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Sequence 88, Application US/10343319
Publication No. US20040072242A1
                                                                                                                                                                                                                                                                             US-10-343-319-87
Sequence 87, Application US/10343319
Publication No. US20040072242A1
GENERAL INFORMATION:
                                                                                                                                                                  16 GCAAACAGGATTAGATACCC 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Legionella pneumophila
US-10-343-319-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hunter, Neil
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                          Query Match
Best Local Similarity
Matches 20; Conserva
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Best Local Similarity
Matches 20; Conserve
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Matches 2
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                                  100.0%; Score 20; DB 12; Length 50; 100.0%; Pred. No. 0.024;
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                                                                                                                                                                                                                                                                           US-10-43-319-84

Sequence 84, Application US/10343319

Publication No. US20040072242A1

GENERAL INFORMATION:

APPLICANT: Hunter, Neil

APPLICANT: Hartin, Fielda E.

APPLICANT: Martin, Fielda E.

APPLICANT: Martin, Fielda E.

TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS

FILE REFERENCE: DAVI139.00249.

CURRENT PAPLICATION NUMBER: US/10/343,319

CURRENT FILING DATE: 2003-09-17

PRIOR APPLICATION NUMBER: AU PQ9090/2000

PRIOR FILING DATE: 2001-07-27

PRIOR FILING DATE: 2000-07-28

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 106

SEQTRARE: FastERO for Windows Version 4.0

SEQTRARE: FastERO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Duricet, Wicholas A.
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Martin, Fjelda E.
APPLICANT: Nardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REPERENCE: DAVI139,002APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2003-09-17
PRIOR PILING DATE: 2001-07-27
PRIOR PILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 106
SEQ ID NOS: 106
SEQ ID NO SE
LENGTH: 50
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                                                                                   0; Indels
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                                                                                   0; Mismatches
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Pred. No. 0
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Publication No. US20040072242A1
GENERAL INFORMATION:
APPLICANT: HUNCEY, Neil
                                                                                                                                  1 GCAAACAGGATTAGATACCC 20
                                                                                                                                                                       16 GCAAACAGGATTAGATACCC 35
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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ORGANISM: Escherichia coli
US-10-343-319-84
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ORGANISM: Salmonella typhi
                                                                                   20; Conservative
                                                         Best_Local Similarity
Matches 20; Conserv
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US-10-343-319-85
                                       Query Match
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                RESULT 15
US-10-343-319-89
i Sequence 89, Application US/10343319
j Publication No. US20040072242A1
j GENERAL INFORMATION:
j APPLICANT: Hunter, Nail
j APPLICANT: Martin, Fjelda E.
j APPLICANT: Martin, Fjelda E.
j APPLICANT: Martin, Fjelda E.
j APPLICANT: Martin, Elelda E.
j APPLICANT: Martin, Elelda E.
j TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS FILE REFERENCE: DAVI139.002APC
j CURRENT APPLICATION NUMBER: US/10/343,319
cURRENT FILING DATE: 2003-09-17
pRIOR APPLICATION NUMBER: PCT/AU01/00933
pRIOR FILING DATE: 2000-07-27
pRIOR FILING DATE: 2000-07-28
j PRIOR FILING DATE: 2000-07-28
j NUMBER: PS SEQ ID NOS: 106
j SEQ ID NO 89
j LENGTH: 50
j TYPE: DNA
j ORGANISM: Nitrobacter winogradskyi
US-10-343-319-89
16 GCAAACAGGATTAGATACCC 35
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Search completed: August 4, 2004, 11:56:21 Job time: 180.964 secs 16 GCAAACAGGATTAGATACCC 35 g

1 GCAAACAGGATTAGATACCC 20

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Sequence 15935, Sequence 72402,

Sequence 297, App Sequence 28084, A Sequence 5759, Ap Sequence 5759, Ap Sequence 5759, Ap Sequence 504, App Sequence 504, App Sequence 506, App Sequence 508, App Sequence 508, App Sequence 503, App Sequence 6938, Ap Sequence 6939, App Sequence 14381, Ap Sequence 2152, Ap Sequence 2152, Ap Sequence 2152, Ap Sequence 2377, Ap

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US-09-940-860-2

Sequence 2, Application US/09940860

Publication No. US2040005555A1

GENERAL INFORMATION:

APPLICANT: Rothman, Richard

APPLICANT: Majmudar, Maulik

TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA

FILE REFERENCE: 01107.00185

CURRENT FILING DATE: 2001-08-29

PRIOR FILING DATE: 2000-08-29

PRIOR FILING DATE: 2000-08-31

PRIOR FILING DATE: 2000-08-31

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 4.0
3 US-10-425-114-15476
3 US-10-425-114-13138
3 US-10-425-114-3138
3 US-10-437-963-72402
3 US-10-437-963-72402
3 US-10-437-963-72402
4 US-10-437-963-26084
4 US-09-923-876-5759
4 US-09-923-876-5759
4 US-09-923-876-5759
4 US-09-922-293-989
5 US-09-922-293-989
5 US-09-922-293-989
5 US-09-922-293-989
5 US-09-922-293-504
5 US-09-922-293-508
5 US-09-847-383-7997
5 US-09-914-353-7997
7 US-09-914-353-7997
7 US-09-938-8428-2377
7 US-09-938-8428-2377
7 US-09-938-8428-2377
7 US-10-77-632-236613
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US-09-940-860-7
Sequence 7, Application US/09940860
Publication No. US2004000555541
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 20; Conservative
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Sequence 11, Appli
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Sequence 11, Appli
Sequence 5, Appli
Sequence 4575, Appli
Sequence 4575, Appli
Sequence 4673, Appli
Sequence 32946, Appli
Sequence 32781, Appli
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Sequence 32781, Appli
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Sequence 25403, Appli
                                                                                                                                   August 4, 2004, 07:44:29; Search time 180.964 Seconds (without alignments) 541.892 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: \cgn2 = \producta/2/\pubpna/USO7 \text{PUBCOMB.seq:*}

2: \cgn2 = \producta/2/\pubpna/USO7 \text{PUBCOMB.seq:*}

3: \cgn2 = \producta/2/\pubpna/USO6 \text{NEW PUB.seq:*}

4: \cgn2 = \producta/2/\pubpna/USO6 \text{PUBCOMB.seq:*}

4: \cgn2 = \producta/2/\pubpna/USO6 \text{PUBCOMB.seq:*}

5: \cgn2 = \producta/2/\pubpna/USO9 \text{PUBCOMB.seq:*}

7: \cgn2 = \producta/2/\pubpna/USO8 \text{NEW PUB.seq:*}

8: \cgn2 = \producta/2/\pubpna/USO8 \text{NEW PUB.seq:*}

9: \cgn2 = \producta/2/\pubpna/USO8 \text{PUBCOMB.seq:*}

10: \cgn2 = \producta/2/\pubpna/USO9 \text{PUBCOMB.seq:*}

10: \cgn2 = \producta/2/\pubpna/USO9 \text{PUBCOMB.seq:*}

11: \cgn2 = \producta/2/\pubpna/USO9 \text{NEW PUB.seq:*}

12: \cgn2 = \producta/2/\pubpna/USO9 \text{NEW PUB.seq:*}

13: \cgn2 = \producta/2/\pubpna/USO9 \text{NEW PUB.seq:*}

14: \cgn2 = \producta/2/\pubpna/USO9 \text{NEW PUB.seq:*}

15: \cgn2 = \producta/2/\pubpna/USO9 \text{NEW PUB.seq:*}

16: \cgn2 = \producta/2/\pubpna/USO9 \text{NEW PUB.seq:*}

16: \cgn2 = \producta/2/\pubpna/USO0 \text{NEW PUB.seq:*}

17: \cgn2 = \producta/2/\pubpna/USO0 \text{NEW PUB.seq:*}

18: \cgn2 = \producta/2/\pubpna/USO0 \text{NEW PUB.seq:*}

19: \cgn2 = \product
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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11 US-09-940-860-7

11 US-09-940-860-7

11 US-09-940-860-5

11 US-09-940-860-5

13 US-10-289-762-1

13 US-10-289-762-1

13 US-10-437-963-4673

14 US-10-437-963-4673

15 US-10-437-963-4673

16 US-10-437-963-861

17 US-10-437-963-861

18 US-10-425-114-32781

19 US-10-369-499-35514

11 US-10-369-499-35514

13 US-10-425-114-25403
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                                                                                                                                                                                                                                                                                                                                     3222919 segs, 2451570024 residues
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                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                  ggaggaaggcgaggatgacg 20
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Maximum DB seq length: 2000000000
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Match Length
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117
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Database :

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Sequence:

Title:

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100.0%; Score 20; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09726774

Patent No. US200208226A1

GENERAL INFORMATION:

APPLICANT: IVESEN, Patrick L.

TITLE OF INVENTION: Antisense Antibacterial Method and
TITLE OF INVENTION: Composition

FILE REFERENCE: 0450-0032.30

CURRENT APPLICATION NUMBER: US/09/726,774

CURRENT APPLICATION NUMBER: US 60/168,150

PRIOR FILING DATE: 1999-11-29

NUMBER OF SEQ ID NOS: 139

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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Publication No. US20040137485A1
GENERAL INFORMATION:
TTILE OF INVENTION: Patrick L.
TTILE OF INVENTION: Composition
FILE REFERENCE: 0450-0032.30
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US/10/719,633
CURRENT APPLICATION NUMBER: US/09/726,774
PRIOR APPLICATION NUMBER: US/09/726,774
PRIOR APPLICATION NUMBER: US 60/168,150
PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 139
APPLICANT: Rothman, Richard
APPLICANT: Majmudar, Maulik
TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
FILE REPERENCE: 01107.00185
CURRENT APPLICATION NUMBER: US/09/940,860
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/229,376
PRIOR FILING DATE: 2000-08-31
                                                                                                                                                                                                                                                                                                               FEATURE:

GOTHER INFORMATION: Synthetic amplification primer
US-09-940-860-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20; DB 9;
Pred. No. 0.049;
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                                                                                                                                                                         NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 30
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CRGANISM: Chlamydia trachomatis
US-09-726-774-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-719-633-11
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APPLICANT: Griffals, R.

IITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

IITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve

IITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/10/289,762

CURRENT FILING DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 6849
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Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-940-960-5
US-09-940-960-5
Sequence 5, Application US/09940860
Publication No. US200400055531
GENERAL INFORMATION:
APPLICANT: Rothman, Richard
APPLICANT: Rothman, Maulik
TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
FILE REFERENCE: 01107.00185
CURRENT APPLICATION NUMBER: US/09/940,860
CURRENT APPLICATION NUMBER: 60/229,376
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11 LENGTH: 1548
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Publication No. US20040006218A1
GENERAL INFORMATION:
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LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or g
                                                                                  ; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-10-719-633-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Chlamydia trichomatis
US-09-940-860-5
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ORGANISM: Chlamydia pneumoniae
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NAME/KEY: misc_feature
LOCATION: (1)...(15000)
OTHER INFORMATION: n=a or c
FEATURE:
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us-09-940-860-2.oligo.rnpb

FEATURE:
NAME/KRY: misc feature
LCCATION: (330001)..(345000)
OTHER INFORMATION: n=a or c or g or t PERTURE:
NAME: MANGE feature
LCCATION: (375001)..(390000)
OTHER INFORMATION: n=a or c or g or t OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (49501)..(510000) JTHER INFORMATION: n=a or c or g or NAME/KEY: misc feáture LOCATION: (570001)..(585000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (420001)..(435000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (390001)..(405000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (510001)..(525000) OTHER INFORMATION: n=a or c or g FEATURE:
NAME/KEY: misc\_feature
LOCATION: (555001)..(570000)
OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (315501)..(330000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc\_feature LOCATION: (360001)..(375000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (435001)..(450000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc\_feature LCCATION: (450001)..(465000) OTHER INFORMATION: n=a or c or g FEATURE: NAME/KEY: misc feature LOCATION: (480001)..(495000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (46501)..(480000) OTHER INFORMATION: n=a or c NAME/KEY: misc feature LOCATION: (405001)..(420000) OTHER INFORMATION: n=a or c NAME/KEY: misc feature LOCATION: (525001)..(540000) OTHER INFORMATION: n=a or c NAME/KEY: misc feature LOCATION: (54001)..(555000) OTHER INFORMATION: n=a or c NAME/KEY: misc feature LOCATION: (345001)..(360000) OTHER INFORMATION: n=a or c NAME/KEY: misc feature LOCATION: (270001)..(285000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (28501)..(300000) OTHER INFORMATION: n=a or c or g or t LOCATION: (30001)..(45000) OTHER INFORMATION: n=a or c or g or WANE/KEY: misc feature LOCATION: (150001)..(165000) THER INFORMATION: n=a or c or g or or ö or ör or ö ö FEATURE: NAME/KEY: misc\_feature LOCATION: (225001)...(240000) OTHER INFORMATION: n=a or c or g FEATURE:
NAME/KEY: misc\_feature
LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (75001)..(90000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (90001). (105000) JTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (105001)..(120000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (120001)..(135000) THER INFORMATION: n=a or c or g NAME/KEY: misc feature CCATION: (165001)..(180000) THER INFORMATION: n=a or c or g AAME/KEY: misc feature OCATION: (180001)..(195000) OTHER INFORMATION: n=a or c or g VAME/KEY: misc feature LOCATION: (210001)..(225000) VTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (240001)..(255000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc\_feature LOCATION: (135001)..(150000) OTHER INFORMATION: n=a or c or FRAMURE: FEATURE:
NAME/KEY: misc\_feature
LOCATION: (25501)..(270000)
OTHER INFORMATION: n=a or c or FEATURE:
NAME/KEY: misc feature
NOCATION: (45001): (60000)
OTHER INFORMATION: n=a or c or or NAME/KEY: misc feature LOCATION: (195001)..(210000) OTHER INFORMATION: n=a or c NAME/KEY: misc\_feature LOCATION: (300001)..(315000)

FEATURE:

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APPLICANT: Lar Rosa, Thomas J.
APPLICANT: Lar Rosa, Thomas J.
APPLICANT: Lar Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: W. Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 4673
LENGTH: 1143
                                                                                                                                                                                                                                                                                             APPLICANT: L1, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(33221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 25445
LENGTH: 2738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Clone ID: PAT_MRT4530_30330C.1
US-10-437-963-25445
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US-10-437-963-4673
                       Sequence 25445, Application US/10437963
PUDIcation No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4673, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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Best Local Similarity 100./
Matches 18; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Oryza sativa
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| Publication No. US20040034888A1
| Publication No. US20040034888A1
| GENERAL INFORMATION:
| APPLICANT: Liu, Jingdong
| APPLICANT: Zhou, Yihua
| APPLICANT: Screen, Serven E
| APPLICANT: Tabaska, Jack E
| APPLICANT: Gao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Nucleic Acid Molecules and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: NUMBER: US/10/425,114
| CURRENT APPLICATION NUMBER: 2003-04-28
| VANDER OF SEQ ID NOS: 73128
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90.0%; Score 18; DB 13; Length 2123;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 18; Conservative 0; Mismatches 0; Indels (
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US-10-425-114-4575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1011866 GGAGGAAGGCGAGGATGACG 1011885
NAME/KEY: misc feature
LOCATION: (58501)..(600000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                       NAME/KEY: misc feature
LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (64501)..(660000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
LOCATION: (67501)..(690000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
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LOCATION: (660001)..(675000)
OTHER_INFORMATION: n=a or c or g or
                                                                                                                                                                                              FEATURE:
NAME/KEY: misc feature
LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g
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Matches 20; Conservative
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ORGANISM: Zea mays
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LENGTH: 2123
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Query Match

Matches

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Gaps

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RESULT 10

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HINKLE, Gregory J.

APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianteng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US(10/369,493)
CURRENT FILING DATE: 2003-02-28
FRIOR PLING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 35514
LENGTH: 2145
TYPE: NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25403, Application US/10425114

| Sequence 25403, Application No. US20040034888A1
| Publication No. US20040034888A1
| GENERAL INFORMATION:
| APPLICANT: Liu, Jingdong
| APPLICANT: Chou, Yimha |
| APPLICANT: Coo, Yongwen |
| APPLICANT: Coo, Yongwen |
| APPLICANT: Coo, Yongwen |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement |
| TITLE OF INVENTION: DAMES: US/10/425,114 |
| CURRENT APPLICATION NUMBER: US/10/425,114 |
| CURRENT PILING DAME: 2003-04-28 |
| SEQ ID NO 25403 |
| LEASTH STATE OF SEQ ID NOS: 73128 |
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100.0%; Pred. No. 11;
.ive 0; Mismatches 0; Indels
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100.0%; Pred. No. ...
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APPLICANT: Amnd; Liangsu
APPLICANT: Amondic, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karii
APPLICANT: Ohlsen, Wali, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0°,
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Mesorhizobium loti
US-10-369-493-35514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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ORGANISM: Zea mays
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Sequence 32781, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Avail, Javid K.

APPLICANT: Cac, Yongwei

APPLICANT: Cac, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 32781

LEMSTH: 2124
                                                                                                                                                                                                                                                       Sequence 32946, Application US/10425114
Sequence 32946, Application US/10425114
Sequence 32946, Application US/10425114
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lou, Vinda
APPLICANT: Storen, Steven E
APPLICANT: Storen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: GF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
85.0%; Score 17; DB 13; Length 1305;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 17; Conservative 0; Mismatches 0; Indels
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US-10-425-114-32781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; CTHER INFORMATION: Clone ID: UC-ZMFLMO17043F07_FLI US-10-425-114-32946
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US-10-369-493-35514/c
; Sequence 35514, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1122 GAGGAAGGCGAGGATGA 1138
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Best Local Similarity 100.
Matches 17; Conservative
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ORGANISM: Zea mays
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LENGTH: 1305
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Sequence 15476, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Edou, Yihua
APPLICANT: Evoulic, David K.
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska,
APPLICANT: ITAMACK, COLLIA
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Younghous, R.
APPLICANT: You, H.
TILLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERBNCE: ELITEA.034A
CURRENT FILING DATE: 2000-03-21
FRIOR PILING DATE: 2000-03-21
FRIOR PLICATION NUMBER: 60/191,078
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-29
FRIOR FILING DATE: 2000-10-22
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80.0%; Score 16; DB 13; Length 1251;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 16; Conservative 0; Mismatches 0; Indels (
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; OTHER INFORMATION: Clone ID: LIB3060-007-All_FLI
*JS-10-425-114-15476
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; ORGANISM: Cornyebacterium diptheriae
US-10-282-122A-17957
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ORGANISM: Zea mays
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80.0%; Score 16; DB 13; Length 1543;

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100.08; Pre-
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             Best Local Similarity 100.
Matches 16; Conservative
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pna/US102A-C pna/US102B-C pna/US103B-C pna/US104B-C pna/US104A-C pna/US104A-C pna/US104A-C pna/US106-C pna/US106-C pna/US107A-C

Run on:

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| Ggn12_6| prodates | 2 pna / US103A_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US103B_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US103B_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US103B_COMB. seq: |
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| Ggn2_6| prodates | 2 pna / US103B_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US103B_COMB. seq: |
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| Ggn2_6| prodates | 2 pna / US103B_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6001_COMB. seq: |
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| Ggn2_6| prodates | 2 pna / US6001_COMB. seq: |
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| Ggn2_6| prodates | 2 pna / US6001_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6001_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6001_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6001_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6011_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6011_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6012_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6012_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6022_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6023_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6023_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6023_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US6023_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US603_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US603_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US603_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US603_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US603_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US603_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US603_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US603_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US603_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US603_COMB. seq: |
| Ggn2_6| prodates | 2 pna / US603_COMB. seq: 
                                                                                                                                                           August 4, 2004, 06:32:11; Search time 1825.78 Seconds (without alignments) 385.436 Million cell updates/sec
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(ggn2 6/ptodata/2/pna/US06 COMB.seq:*
(ggn2 6/ptodata/2/pna/US08 COMB.seq:*
(ggn2 6/ptodata/2/pna/US081 COMB.seq:*
(ggn2 6/ptodata/2/pna/US082 COMB.seq:*
(ggn2 6/ptodata/2/pna/US089 COMB.seq:*
(ggn2 6/ptodata/2/pna/US099 COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                   - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 1, Appli
Sequence 1, Appli
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Sequence 7, Appli
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Sequence 5,
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GENERAL INFORMATION:
APPLICANT: Rothman, Richard
APPLICANT: Rothman, Richard
TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
FILE REPERENCE: 01107.0185
CURRENT APPLICATION NUMBER: US/09/940,860
CURRENT FILING DATE: 2001-08-29
FIOR APPLICATION NUMBER: 60/229,376
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 20
                                                                                                                                                                                                                                                                                                             US-60-085-146-2609
US-09-280-918A-696
US-60-079-469-696
US-09-873-402A-12532
                                                                                                                                                                             US-10-425-1144-4575
US-10-427-963-25445
US-09-702-1134-21825
US-09-620-392-33867
US-09-256-2184-1587
US-09-255-2184-1587
US-09-955-268-1587
US-09-993-9794-2609
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US-09-849-526A-17839
US-60-202-214-17594
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US-60-202-214-27390
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US-60-207-458-29567
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US-10-425-114-4575
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                                                                                               US-09-201-228A-1
US-10-289-762-1
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US-09-438-185A-1
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ORGANISM: Artificial Sequence
FEATURE:
Query
Match Length
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US-09-940-860-2
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Result
No.
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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                            39; Length 20;
                                                                                                                                                      Indels
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US-10-719-633-11
Sequence 11, Application US/10719633
Sequence 11, Application US/10719633
Sequence 11, Townstain Methors
TITLE NPORMATION:
TITLE OF INVENTION: Antisense Antibacterial Method and
TITLE OF INVENTION: Composition
FILE REFERENCE: 0450-0032.30
CURRENT PILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US/09/726,774
PRIOR PILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH 1548
                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-09-940-960-7
US-09-940-60-7
Sequence 7, Application US/09940860
Sequence 7, Application US/09940860
Sequence 7, Application US/09940860
TO SEQUENCE 1 Sequence 7, Application 1 Sequence 7, Applicant 8
TILE REPERBING: MAULIK
TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
TITLE OF INVENTION: WOLECULAR DIAGNOSIS OF BACTEREMIA
TITLE OF INVENTION NUMBER: US/09/940,860
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/229,376
PRIOR APPLICATION NUMBER: 60/229,376
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-460-7
; OTHER INFORMATION: synthetic amplification primer US-09-940-860-2
                                                                                      Query Match 100.0%; Score 20; DB Best Local Similarity, 100.0%; Pred. No. 2; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1179 GGAGGAAGGCGAGGATGACG 1198
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, ORGANISM: Chlamydia trachomatis
US-10-719-633-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 7
LENGTH: 30
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Sequence 1. Application US/10289762

Sequence 1. Application US/10289762

GENERAL INFORMATION:

APPLICANT: Griffais, F.

TILLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment:
TILLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, previritle OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/10/289,762

CURRENT FILING DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1

LENGTH: 1230025
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NAME/KEY: misc_feature
LOCATION: (75001)..(90000)
THER INFORMATION: n=a or c or g or
FEATURE:
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LOCATION: (120001)..(135000)
OTHER INFORMATION: n=a or c or g or
FEATURE:
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LOCATION: (180001)..(195000)
OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g
FEATURE:
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LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (165001)..(180000)
OTHER INFORMATION: n=a or c or
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LLOCATION: (15001)..(30000)
OCHER INFORMATION: n=a or c or
PEATURE:
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LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or
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CCCATION: (135001)..(150000)
OTHER INFORMATION: n=a or c or
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Chlamydia pneumoniae
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LOCATION: (150001)..(165000)
OTHER INFORMATION: n=a or c
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LOCATION: (195001)..(210000)
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LOCATION: (90001)..(105000)
OTHER INFORMATION: n=a or c
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LOCATION: (30001)...(45000)
OTHER INFORMATION: n=a or
FEATURE:
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LOCATION: (45001)..(60000)
OTHER INFORMATION: n=a or
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NAME/KEY: misc_feature
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APPLICANT: Griffais, Remy
APPLICANT: Agairsky, Robert John
APPLICANT: Agairsky, Robert John
APPLICANT: Becalf, Benjamin J.
APPLICANT: Beck, Joel A.
APPLICANT: Peck, Joel A.
TITLE OF INVENTION: CHLAMYDIA TRACHOMATIS GENOMIC SEQUENCE
TITLE OF INVENTION: AND POLYPEPTIDES, FRACHENTS THEREOF AND USES THEREOF, IN
TITLE OF INVENTION: NPECTION
TITLE OF INVENTION: INFECTION
FILE REFERENCE: 9710-0004-99
CURRENT APPLICATION NUMBER: US 60/107,077
PRIOR PELICATION NUMBER: FR 97-16034
PRIOR PELING DATE: 1998-11-04
PRIOR PELING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: FR 97-15041
PRIOR PILING DATE: 1997-11-28
NUMBER OF SEQ ID NOS: 5981
SOFTWARE: FRAESEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                APPLICANT: Najmudar, Maulik
APPLICANT: Majmudar, Maulik
TITLE OP INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
FITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
FILE REFERENCE: 0.1107 0.0185
CURRENT APPLICATION NUMBER: 0.8/09/940,860
CURRENT FILING DATE: 2.001-08-29
PRIOR APPLICATION NUMBER: 60/229,376
PRIOR PILING DATE: 2.000-08-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1550
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GENERAL INFORMATION:
APPLICANT: Griffais, Remy
APPLICANT: Hoiseth, Susan K.
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OTHER INFORMATION: n = A,T,C or G
US-09-201-228A-1
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                      Sequence 5, Application US/09940860 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
; ORGANISM: Chlamydia trichomatis
US-09-940-860-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
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LENGTH: 1038608
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-09-940-860-5
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FEATURE:
NAME/KEY: misc feature
LOCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or g or t
FEATURE: misc feature
LOCATION: (225001)..(240000)
OTHER INFORMATION: n=a or c or g or t FEATURE:
NAME/KEY: misc feature
LOCATION: (240001)..(255000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (465001)..(480000) OTHER INFORMATION: n=a or c or g or t FEATURE:
NAME/KEY: misc\_feature
COCA\_TROY (270001)..(285000)
OTHER INFORMATION: n=a or c or g or t FRATURE:
NAME/KFY: misc\_feature
LCCATION: (37501)..(390000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (420001)..(435000) DTHER INFORMATION: n=a or c or g or t or t or t FEATURE:
NAME/KEY: misc\_feature
LOCATION: (255001)..(270000)
OTHER INFORMATION: n=a or c or g or or NAME/KEY: misc feature LOCATION: (330001)..(345000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (390001)..(405000) THER INFORMATION: n=a or c or g or or 占 FEATURE:
MAMP/KEY: misc\_feature
LOCATION: (315001).,(330000)
OTHER INFORMATION: n=a or c or g NAME/KEY: misc\_feature LOCATION: (285001)..(300000) JTHER INFORMATION: n=a or c or g FEATURE:
NAME/KEY: misc\_feature
COCATION: (300001)..(315000)
CTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (360001)..(375000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (405001)..(420000) JTHER INFORMATION: n=a or c or g NAME/KEY: misc\_feature LOCATION: (43501)...(450000) OTHER INFORMATION: n=a or c or g OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (345001)..(360000) OTHER INFORMATION: n=a or c NAME/KEY: misc feature LOCATION: (45001)..(465000) OTHER INFORMATION: n=a or c

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Gaps
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100.0%; Score 20; DB 48; Length 1230025;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1011866 GGAGGAAGGCGAGGATGACG 1011885
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NAME/KEY: misc_feature
LOCATION: (67501)...(690000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
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NAMEN MISC. feature
NAMEN ($10001)...($25000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (615\overline{0}01)..(630000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (525001)..(540000)
DTHER INFORMATION: n=a or c or g or
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LOCATION: (570001)..(585000)
OTHER INFORMATION: n=a or c or g or
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NAME/KEY: misc feature
LCOATION: (58501)..(60000)
OTHER INFORMATION: n=a or c or g or
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FEATURE:
NAME/KEY: misc feature
LOCATION: (48001)..(495000)
OTHER INFORMATION: n=a or c or g or
FEATURE:
NAME/KEY: misc_feature
LOCATION: (495001)..(510000)
OTHER INFORMATION: n=a or c or g or
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NAME/KEY: misc_feature
NAME/KEY: wisc_feature
(S40001)..(555000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g
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NAME/KEY: misc_feature
NAME/KEY: misc_feature
OCATION: (64501)..(660000)
OTHER INFORMATION: n=a or c or
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LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c
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LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c
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NAME/KEY: misc feature
LOCATION: (55501)..(57000)
OTHER INFORMATION: n=a or c
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RESULT 7
US-09-438-185-1
US-09-438-185-1
; GEQUENCE 1, Application US/09438185
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard

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Sequence 4575, Application US/10425114

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Cao, Yihua
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE REPERBENCE: 38-21(5313)8
CURRENT APPLICANTON NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
IUBMER OF SEQ ID NOS: 73128
LENGTH: LENGTH:
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| Sequence 4575, Application US/10425114A
| SENERAL INFORMATION:
| APPLICANT: Liu, Jingdong
| APPLICANT: Zhou, Yihua
| APPLICANT: Sereen, Ser
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 47; Length 2123;
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                        FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR PILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 18302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: 700382382_FLI
US-10-425-114-4575
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Pred. No.
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100.0%; Pre
0; 1
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Best Local Similarity 100.0%; P:
Matches 18; Conservative 0;
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Best Local Similarity 100.0
Watches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION; (161)..(1768)
; OTHER INFORMATION:
US-10-219-999-18302
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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100.0%; Score 20; DB 20; Length 1230230;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0;
                                   APPLICANT: Kalman, Sue
APPLICANT: Kalman, Sue
APPLICANT: Raiman, Sue
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REPERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185
CURRENT FILING DATE: 1999-11-11
PRIOR APPLICATION NUMBER: US 60/108,279
FRIOR FILING DATE: 1999-04-08
NUMBER OF FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 1230230
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APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
CURRENT APPLICANION NUMBER: US/09/438,185A
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PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: PastSEQ for Windows Version 3.0
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-438-185-1
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ORGANISM: Chlamydia pneumoniae
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APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-219-999-18302/c
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LENGTH: 1230230
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US-09-815-264-71774/C

Sequence 71774, Application US/09815264

GENERAL INFORMATION:
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Cot, Yongwei
APPLICANT: Cotson, Stanton B.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Mu, Wei
APPLICANT: McIninch, James
APPLICANT: Mu, Wei
APPLICANT: Mu, Wei
CURRENT PLING BATE: 2001-03-23
FRIOR PILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669

SEQ ID NO 71774
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                                                                                                                                  Query Match 90.0%; Score 18; DB 30; Length 13218; Best Local Similarity 100.0%; Pred. No. 17; Matches 18; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 90.0%; Score 18; DB 33; Length 13218; Best Local Similarity 100.0%; Pred. No. 17; Matches 18; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: McIninch, James
TITLE OF INVENTION: 38-21 (51237) E
FILE REPERBENCE: 38-21 (51237) E
CURRENT APPLICATION NUMBER: US/09/620,392
CURRENT FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 69652
SEQ ID NO 33867
LENGTH: 13263
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                                                                                                                                                                                                                                                                                    1 GGAGGAAGGCGAGGATGA 18
                                                                                                                                                                                                                                                                                                                                                   103 GGAGGAAGGCGAGGATGA 86
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; TYPE: DNA; ORGANISM: Oryza sativa
US-09-702-134-21825
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; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-815-264-71774
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US-09-620-392-33867/c
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Sequence 25445, Application US/10437963
General Properation:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boucharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
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US-10-437-963-25445
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GENERAL INFORMATION:
APPLICANT:
BOUNCARCY, Andrey A.
APPLICANT:
APPLICANT:
Coo, Yongwei
APPLICANT:
APPLICANT:
MU, Vingdong
APPLICANT:
MU, Wei
TILE OF INVENTION
TILLE OF INVENTION:
TILLE OF INVENTION
CURRENT APPLICATION NUMBER: US/09/702,134
CURRENT FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 52202
SEQ ID NO 21825
LENGTH: 13218
                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Clone ID: 700382382_FLI
US-10-425-114A-4575
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 4575
LENGTH: 2123
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ORGANISM: Oryza sativa
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                              3470272 seqs, 21671516995 residues
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22
1 acaaggcccgagaacgtattca 22
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Gapop_60.0 , Gapext 60.0
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AF294958 Unculture AF396905 Unculture AF391643 Unculture AF391670 Unculture AF391670 Unculture AF371569 Sequence AF371569 Sequence AF371569 Sequence AF3721480 Unidentif AF254201 Unculture AF295281 Unculture AF295281 Unculture AF295281 Unculture AF39528 Wobiluncu AF39528 Wobilure AF39528 Wobilure AF39528 Wobilure AF3918 Unculture AF391918 Unculture AF391918 Unculture AF49786 Unculture AF49786 Unculture AF49786 Unculture AF49786 Unculture AF42914 Unculture AF42914 Unculture AF429234 Unculture AF42914 Unculture AF322096 Unculture AF32096 Unculture AF322096 Unculture AF322096 Unculture AF322096 Unculture AF322096 Unculture AF322096 Unculture	DNA linear BCT 10-JAN-2002 ribosomal RNA gene, partial RNA gene, p
SUMMARIES B ID	AF294958 AF289905 AF28990637 AY391643 AY391643 AY391643 AY391643 AY391643 AY391643 AY391644 AY391644 AY191889 AF257294 AY191889 AF257294 AY191889 AF261424 AF261428 AF261424 AF429144 AF429144 AF429144 AF429144 AF429234 AF4292631 AF4292631 AF422631	ALIGNMENTS 236 bp TUI 16S rib samples. Sowers, K.R. sorganism t of 2,3,5,6
* Query Match Length Di	200 000 000 000 000 000 000 000 000 000	AP294958 Uncultured eubacterium O' sequence. AP294958.1 GI:15419629 uncultured eubacterium I (bases I to 236) Cutter, L.A., Matts, J.E., Identification of a micro reductive dechlorination
Result No. Score	0000000 00000 00000000 0 0 00000000000	RESULT 1 AF24958/C LOCUS DEFINITION UNC ACCESSION AFY VERSION AND ANTHORS TITLE TER

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260 bp DNA linear BCT 10-FEB-2002
Uncultured green sulfur bacterium clone OTU 1 16S ribosomal RNA
AP389905
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                                                       Cuterina, Watts, J.E.M., Sowers, K.R. and May, H.D.
Indications for actate as the carbon source and electron donor in
anaerobic ortho PCB dechlorination
Unpublished
J (bases I, Cutter, L.A., Sowers, K.R. and May, H.D.

Direct Submission
Submitted (11.4022000) Center of Marine Biotechnology, 701 E.

Pratt St., Baltimore, MD 21202, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (11-JUN-2001) Center of Marine Biotechnology, University of Maryland Biotechnology Institute, Columbus Center, 701 E. Pratt St., Baltimore, MD 21202, USA
Location/Qualifiers
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uncultured Chlorobi paterium
Bacteria, Chlorobi, environmental samples.

1 (bases 1 to 260)
w.Q., Watts, J.E., Sowers, K.R. and May, H.D.
Identification of a bacterium that specifically catalyzes the
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/db.xref="taxon:156405"
/clone="GNU 1"
/note="DNA sequence from PCB-dechlorinating enrichment
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                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:73429"
/note="OTU 1; PCB dechlorinating culture"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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21681065
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Environ. Microbiol. 3 (11), 699-709 (2001)
21835716
11846760
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/product="168 ribosomal RNA"
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/product="16S ribosomal RNA"
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uncultured soil bacterium

Sw uncultured soil bacterium

Bacteria; environmental samples.

E (bases 1 to 302)

Sun, H., Deng, Sand Raun, W.R.

Microbiology community structure and diversity in a century-long manure-treated agroecosystem

L Unpublished

Sun, H., Deng, Sand Raun, W.R.

Sun, H., Deng, Sand Raun, W.R.

Sun, H., Deng, Sand Raun, W.R.

Direct Submission

L Submitted (16-SEP-2003) Plant and Soil Sciences, Oklahoma State University, 368 Ag Hall, Stillwater, OK 74078, USA
                                                                                                                                       AY391637 302 bp DNA linear BCT 15-OCT-2003
Uncultured soil bacterium clone M21 16S ribosomal RNA gene, partial
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Uncultured soil bacterium clone M27 168 ribosomal RNA gene, partial
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Sun, H., Deng, S. and Raun, W.R.
Microbiology community structure and diversity in a century-long manure-treated agroecosystem
manure-treated agroecosystem
tupublished
2 (bases 1 to 302)
Sun, H., Deng, S. and Raun, W.R.
Direct Submission
Submitted (16-SEP-2003) Plant and Soil Sciences, Oklahoma State University, 368 Ag Hall, Stillwater, OK 74078, USA
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/mol type="genomic DNA"
/isolation_source="total microbial community of
century-long manure-treated soil"
/db xeef="taxon:164851"
/clone="M21"
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100.0%; Score 22; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 22; Conservative 0; Mismatches 0; Indels
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/product="168 ribosomal RNA"
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AY391637.1 GI:37624038
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372 bp DNA linear BCT 09-JUL-2001
Uncultured marine gamma proteobacterium DHB-31 16S ribosomal RNA
Gene, partial sequence.
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[Description 1972]
[Description 1972]
[Diversity of free-living prokaryotes from a deep-sea site at the Antarctic Polar Front
FEMS Microbiol. Ecol. 36 (2-3), 193-202 (2001)
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Submitted (18-APR-2000) Microbiology, University Miguel Hernandez,
Facultad de Medicina, Campus de San Juan, San Juan, Alicante 03550,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="uncultured marine gamma proteobacterium DHB-31"
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uncultured marine gamma proteobacterium DHB-31
Bacteria; Proteobacteria; Gammaproteobacteria; environmental
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                                                                                                                                               100.0%; Score 22; DB 6; Length 368; 100.0%; Pred. No. 3.9; cive 0; Mismatches 0; Indels
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100.0%; Score 22; DB 6;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 22; Conservative 0; Mismatches 0;
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1 (bases 1 to 370)

Dodge,D.E. and White,T.J.

Method for diagnosis of lyme disease

Patent: US 5912117-A 35 15-JUN-1999;

Location/Qualifiers
Method for diagnosis of lyme disease
Patent: US 5912117-A 36 15-JUN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    AR071568 370 bp 1
Sequence 35 from patent US 5912117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unknown"
/mol_type="unassigned DNA"
                                                       1. .368
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                              273 ACAAGGCCCGAGAACGTATTCA 252
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ARO71568.1 GI:7222456
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                                                                                                                                                                 1 Similarity 100.
22; Conservative
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AF257294/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uncultured soil bacterium
SM uncultured soil bacterium
Bacteria; environmental samples.
E. 1 (bases 1 to 309)
S. Sun, H., Deng, S. and Raun, W.R.
Microbiology community structure and diversity in a century-long manure-treated agroecosystem
L. Unpublished
E. 2 (bases 1 to 309)
S. Sun, H., Deng, S. and Raun, W.R.
Direct Submission
L. Sun, H., Deng, S. and Raun, W.R.
Direct Submission
L. Sun, H., Seng, S. and Raun, W.R.
Direct Submission
L. Sun, H., Sand, M.R.
Sun, H., Seng, S. and Raun, W.R.
Direct Submission
L. Sun, H., Stillwater, OK 74078, USA
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Uncultured soil bacterium clone M54 16S ribosomal RNA gene, partial
sequence.
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/isolation_source="total microbial community of century-long manure-treated soil"
/db_xref="taxon:164851"
 /isolation_source="total microbial community of
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100.0%; Score 22; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 22; Conservative 0; Mismatches 0; Indels
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             century-long manure-treated soil"
/db xref="taxon:164851"
/clone="M27"
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/product="16S ribosomal RNA"
                                                                                            <li..>302
/product="168 ribosomal RNA"
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Sequence 36 from patent US 5912117.
AR071569.1 GI:7222457
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Unclassified.
1 (bases 1 to 368)
Dodge, D.E. and White, T.J.
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Uncultured euglenid clone CD1H11 168 ribosomal RNA gene, partial
sequence.
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Unidentified microorganism 16S rRNA gene, partial, clone Cow39.
AJ241780
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Submitted (14-APR-1999) Pryde S.E., Microbial and Intestinal
biology, Rowett Research Institute, Greenburn Road, Bucksburn,
Aberdeen, AB21 9SB, UK
Location/Qualifiers
                                                                                                                                  Gaps
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(Dasse: 1 to 380)

Pryde, S.E., Richardson, A.J., Stewart, C.S. and Flint, H.J. Molecular analysis of the microbial diversity present in the colonic wall, colonic lumen, and cecal lumen of a pig Appl. Environ. Microbiol. 65 (12), 5372-5377 (1999)
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uncultured euglenid
Eukaryota; Euglenozoa; environmental samples.
I (bases 1 to 420)
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ilarity 100.0%; Pred. No. 3.9;
Conservative 0; Mismatches 0;
                                            <1. .>372
/product="16S ribosomal RNA"
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/gene="16S rRNA"
/product="16S ribosomal RNA"
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/db_xref="taxon:81726"
/clone="Cow39"
/mol_type="genomic DNA"
/db_xref="taxon:123962"
/clone="DHB-31"
                                                                                                                                                                             259 ACAAGGCCCGAGAACGTATTCA 238
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Pryde, S.E.
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Bacteria; environmental samples.
1 (bases 1 to 431)
Chelius,M.K. and Triplett,E.W.
The Diversity of Archaea and Bacteria in Association with the Roots of Zea mays L
Microb. Ecol. 41 (3), 252-263 (2001)
Frias-Lopez,J., Zerkle,A.L., Bonheyo,G.T. and Fouke,B.W. Partitioning of bacterial communities between seawater and healthy, black band diseased, and dead coral surfaces Appl. Environ. Microbiol. 68 (5), 2214-2228 (2002)
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                                                                                                                            2 (bases 1 to 420)
Frias-Lopez, J., Zerkle, A.L., Bonheyo, G.T. and Fouke, B.W.
Direct Submission
Submitted (06-AUG-2002) Department of Geology, University of
Illinois at Urbana-Champaign, 1301 W. Green Street, Urbana, IL
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    431
    /organism="uncultured maize root bacterium Zmrc163"

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/organism="uncultured euglenid"
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Zmrc163
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/product="16S ribosomal RNA"
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/product="168 ribosomal RNA"
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Chelius, M.K. and Triplett, E.W.
Direct Submission
Submitted (19-JAN-2000) Agronomy, Un
1575 Linden Dr., Madison, WI 53706,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  /mol type="genomic DNA"
/isolation_source="marine"
/db_xref="taxon:167168"
/clone="CD1H11"
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/clone="Zmrc163"
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AF226208
AF226208.1 GI:7716143
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Gaps

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BCT 02-JAN-2003

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497 bp DNA linear BCT 09-APR-2001
Uncultured green nonsulfur bacterium Kmlps6-20 16S ribosomal RNA
Gene, partial sequence.
AF289914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished

2 (bases 1 to 473)

Park, H., Kim, C., Choi, H., Jang, H. and Kim, H.

Direct Submission
Submitted (25-MAY-2001) SJ Hightech Co., Ltd., College of Medicine, Pusan National University, 10 Amidong-1-Ga, Seogu, Pusan 602-739, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Park, H., Kim, C., Choi, H., Jang, H. and Kim, H.
Mobiluncus curtisii DNA for 16S-23S rRNA internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria, Actinobacteridae; Actinomycetales; Actinomycineae; Actinomycetaceae; Mobiluncus.
1 (bases 1 to 473)
                                                                                                                                                                                                                                                                                                                                                                                                  Mobiluncus mulieris 16S-23S ribosomal RNA intergenic spacer.
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                                                                                                                                                                                           Query Match 100.0%; Score 22; DB 1; Length 458; Best Local Similarity 100.0%; Pred. No. 3.7; Matches 22; Conservative 0; Mismatches 0; Indels
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uncultured green non-sulfur bacterium Kmlps6-20
Bacteria, Chloroflexi, environmental samples.
                1. .458
/organism="uncultured bacterium ECS7"
/mol_type="genomic DNA"
/db_xref="taxon:122037"
/clone="ECS7"
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    .473
    organism="Mobiluncus mulieris"

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Pred. No. 3.6;
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/product="16S ribosomal RNA"
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/strain="ATCC35243"
/db_xref="ATC:35243"
/db_xref="taxon:2052"
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Bacterial distribution and phylogenetic diversity in the Changjiang estuary before the construction of the Three Gorges Dam
Microb. Ecol. 43 (1), 82-91 (2002)
                                                       BCT 10-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB041277 458 bp DNA linear BCT 29-NOV-2002 Uncultured bacterium ECS7 gene for 16S ribosomal RNA, partial
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                                                                                                                                                                                                                                                                                                                        Unpublished
To Chases 1 to 432)
Macur.R.E. Languer,H.W. and Inskeep,W.P.
Direct Submission
Direct Submission
Montana State University - Bozeman, Leon Johnson Hall, Bozeman, MT
59717, USA
                                                                                                                                                                  uncultured bacterium
uncultured bacterium
bacteria; environmental samples.
1 (Dases I to 432)
Macur,R.E., Languer,H.W. and Inskeep,W.P.
Molecular analysis of microbial communities in
acid-sulfate-chloride-arsenic geothermal springs in Yellowstone
National Park
                                                   AY191889 432 bp DNA linear BCT 10-MAR Uncultured bacterium clone BG6 168 ribosomal RNA gene, partial
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/mol type="genomic DNA"
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geothermal spring"
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/environmental sample
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llarity 100.0%; Pred. No. 3.7;
Conservative 0; Mismatches 0; Indels
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/product="168 ribosomal RNA"
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uncultured bacterium ECS7
Bacteria, environmental samples.
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AY191889.1 GI:28396218
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AB041277.1 GI:10716064
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Yu, Z. and Mohn, W.W.

Yu, Z. and Mohn, W.W.

Bacterial diversity and community structure in an aerated lagoon revealed by ribosomal intergenic spacer analyses and 168 ribosomal DNA sequencing

Appl. Environ. Microbiol. 67 (4), 1565-1574 (2001)

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12 (Appl. Sequencing of the properties of the propert
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1. 497

/ Organia="uncultured green non-sulfur bacterium Kmlps6-20"

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/db xref="kmlps6-20"

/lone="kmlps6-20"

/lone="kmlps6-20"

/lone="kmlps6-20"

/product="l65 ribosomal RNA"
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Matches 22; Conservative 0; Mismatches 0; Indels
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Search completed: August 4, 2004, 07:44:19 Job time: 965.229 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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August 4, 2004, 04:03:11; Search time 875.663 Seconds (without alignments) 989.948 Million cell updates/sec 6940544 Total number of hits satisfying chosen parameters: 3470272 seqs, 21671516995 residues OM nucleic - nucleic search, using sw model Post-processing: Listing first 45 summaries US-09-940-860-2 20 1 ggaggaaggcgaggatgacg 20 OLIGO NUC Gapop 60.0 , Gapext 60.0 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Title: Perfect score: Scoring table: Word size : Sequence: Searched: Run on:

Database :

em\_in: \*
em\_om: \*
em\_or: \*
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Pred. No. is the number of results predicted by chance to have a

em\_sy:\* em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htgo\_other:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S Description	Endos	Uncult	Candidat	Uncul	Uncul	Uncul	Uncul	Arsz4023 Unculture L35460 Alpha prote	AB088955 Unculture	AF229/91 Unculture AF127027 Helicobac	U73782 Chlamydia p	U/3/85 Chlamydia p U73783 Chlamydia p	AY126640 Endosymbi	AY328728 Unculture	AJ400342 Unculture	AF382141 Unculture	2498/4 C.pneumonia 249871 Chlamydophi	Z49872 Chlamydophi	AF507685 Unculture	075649 Unidentifie 249873 C.pneumonia	AJ408994 Unculture	AY328720 Unculture	ABOUI//8 Chlamydop ABO01779 Chlamydop	AB001780 Chlamydop	AB001781 Chlamydop	ABOO1783 Chlamydop ABO01783 Chlamydop	AB001784 Chlamydop	AB001785 Chlamydop	ABOUL/86 Chlamydop ABO01787 Chlamydop	AB001788 Chlamydop	AB001789 Chlamydop	AB001790 Chiamydop AB001791 Chiamydop	SE	DNA linear BCT 03-APR-1999 uensis gene for 16S ribosomal RNA,		uensis	kiusiuensis ammaproteobacteria; Enterobacteriales; osymbionts; Candidatus Blochmannia.	de,O., Minaka,N. and Matsumoto,T. endosymbionts with their host ants
SUMMARIE	7967	12	AF317470	964	UBA309647	DBA309611 AF050608	UBA519648	AF524023 APBRGDC	AB088955	AF127027	CPU73782	CPU73783	AY126640	AY328728 AF382129	MBA400342	AF382141	CPIOLIBER	CPOAE16SR	AF507685	CPTW183ER	UEU408994	AY328720	AB001778 AB001779	AB001780	AB001781	AB001/82 AB001783	AB001784	AB001785	AB001786 AB001787	AB001788	AB001789	AB001790 AB001791	ALIGNMENT	570 bp DN Camponotus kiusiuensi	18	amponotus kiusiuensis	Jamponotus kiusi Sacteria; Gammap Re; ant endosymb	3., Kita of the
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Length	570	617	827	905	910	936	1247	1298	1313	1335	1354	1355	1383	1433	1446	1447	145/	1466	1468	1471	1480	1492	1507	1507	1507	1507	1507	1507	1507	1507	1507	1507		of GCB	T: 4	) H	of ( teob	Ö.
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Score	0.0	700	50	700	0.0	0 0	20	0 0	50	0 0	20	0 0	200	200	0 0	20	0 0	200	50	0 0	50	0 0	0 0	70	20	0 0	0 0	0 0	N 0	200	20	0 0						
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AF31/47U BCT 04-FEB-2002
Candidatus Helicobacter bovis strain Toro3A.16S ribosomal RNA gene,
partial sequence.
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/strain="Toro3A"
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obtained from the gastric mucosa of a bull from Venezuela"
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
Uncultured bacterium clone F-OTU12 16S ribosomal RNA gene, partial
                                                                                                                            Bacteria; environmental samples.

1 (bases 1 to 617)

2 Analysis of the microbial community composition and transition in the activated sludge of a lab-scale deammonification reactor by
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Gueneau, P., Fuenmayor, J., Aristimuno, O.C., Cedeno, S., Baez, E.,
Reyes, N., Michelangeli, F. and Dominguez-Bello, M.G.
Are goats naturally resistant to gastric Helicobacter infection?
Vet. Microbiol. 84 (1-2), 115-121 (2002)
                                                                                                                                                                                                                                                                           Zheng,X., Yang,H. and Li,D. Direct Submission Submitted (18-AUG-2003) School of Life Science and Technology, Shanghai Jiaotong University, No.800, Dongchuan Road, Shanghai
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/organism="uncultured bacterium"
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Submitted (27-OCT-2000) CBB, IVIC, Km 11
Pipe Miranda, Venezuela
Location/Qualifiers
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100.0%; Pred. No. 40;
iive 0; Mismatches 0;
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/product="16S ribosomal RNA"
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2 (bases 1 to 617)
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Gueneau de Novoa,P.
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Empirical and theoretical bacterial diversity in four Arizona soils
Appl. Environ. Microbiol. 68 (6), 3035-3045 (2002)
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                                                                          Direct Submission
Submitted (14-OCT-1998) Shinya Sameshima, University of Tokyo,
Department of Biology, 3-8-1 Komaba, Meguro-ku, Tokyo 153-8902,
Japan (E-mail:877216@hongo.ecc.u-tokyo.ac.jp, Tel:+81-3-5454-6652,
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Uncultured soil bacterium clone S13 16S ribosomal RNA gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [Dunbar,J., Barns,S.M., Ticknor,L.O. and Kuske,C.R. Dunbar,J., Barns,S.M., Ticknor,L.O. and Kuske,C.R. Direct Submission
Submitted (26-APR-2002) Biosciences Division, Los Alamos National Laboratory, M888, Los Alamos, NM 87545, USA
Location/Qualifiers
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100.0%; Pred. No. 41;
iive 0; Mismatches
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<1._.>570
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1 (bases 1 to 601)
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UBA309647 910 bp DNA linear BCT 06-JUN-2003
Uncultured Chloroflexaceae group bacterium 16S rRNA gene, clone
P6-C12.
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Direct Submission
Direct Submission
Submitted (09-FBB-2001) Nuebel U., Molekulare Systematik und Submitted (09-FBB-2001) Nuebel U., Molekulare Systematik und Schotogie, Deutsche Sammlung von Mikrocrganismen und Zellkulturen, Mascheroder Weg 1B, Braunschweig, 38124, GERMANY
Location/Qualifiers
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Submitted (109-FBB-2001) Nuebel U., Molekulare Systematik und
Submitted (109-FBB-2001) Nuebel U., Molekulare Systematik und
Oekologie, Deutsche Sammlung von Mikroorganismen und Zellkulturen,
Oekologie, Deutsche Sammlung von Mikroorganismen und Zellkulturen,
Mascheroder Weg 1B, Braunschweig, 38124, GERMANY
Location/Qualifiers
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AJ309647.
AJ309647.1 GI:15552893
AJ309647.1 GI:15552893
Informal RNA, 168 rRNA gene.
uncultured Chloroflexales bacterium
uncultured Chloroflexales bacterium
Bacteria; Chloroflexi; Chloroflexales; environmental samples.
Information of the control of th
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100.0%; Score 20; DB 1;
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Uncultured alpha proteobacterium clone WCPAP15 16S ribosomal RNA
AY220719
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Uncultured Chloroflexaceae group bacterium 16S rRNA gene, clone
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Prokaryotic community structure and biodiversity in deep waters of
Prokaryotic community structure and biodiversity in deep waters of
Unpublished
2 (bases 1 to 857)
2 (bases 2 to 857)
2 (bases 3 to 857)
3 (bases 3 to 857)
5 (bases 1 to 857)
6 (17-JAM-2003) Microbiology, NUI, Galway, University Rd.,
Galway, Rep. of Ireland
Galway, Rep. of Ireland
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/isolation source="water column, Porcupine Abyssal Plain,
Northeast Ātlantic Ocean"
/db xref="texon:91750"
/clone="WCPAPIS"
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AJ309645.
AJ309645.1 GT:15552891
Is ribosomal RNA, 16S rRNA gene.
Uncultured Chloroflexales bacterium
SM uncultured Chloroflexies bacterium
Bacteria, Chloroflexi, Chloroflexales, environmental samples.
E 1 (asses 1 to 902)
Nubel, U., Bateson, M.M., Madigan, M.T., Kuhl, M. and Ward, D.M.
Diversity and distribution in hypersaline microbial mats of bacteria related to Chloroflexus spp
Dacteria related to Chloroflexus spp
E 21417071
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Bacteria; Proteobacteria; Alphaproteobacteria; environmental
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Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels
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/product="16S ribosomal RNA"
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                                                                               100.0%; Score 20; DE ilarity 100.0%; Pred. No. 37; Conservative 0; Mismatches
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Uncultured bacterium partial 16S rRNA linear BCT 29-NOV-2002 AJ519648 AJ519648. GI:26005694 16S rRNA gene, clone Sh765B-AG-14. AJ519648.1 GI:26005694 16S ribosomal RNA; 16S rRNA gene. uncultured bacterium uncultured bacterium Bacteriam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geissler, A., Tzvetkova, T., Flemming, K. and Selenska-Pobell, S. Comparison of natural bacterial communities found in uranium mining waste piles and mill tailings
Unpublished
Submitted (24-FEB-1998) Plant and Microbial Biology, University california, Berkeley, 111 Koshland Hall, Berkeley, CA 94720, USA Location/Qualifiers
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Selenaka-Pobell,S.I.
Direct Submission
Submitted (28-NOV-2002) Selenaka-Pobell S.I., Molecular
Microbiology, Institute of Radiochemistry, FZR, P.O.B. 51 01 19,
D-01314 Dresden, GERMANY
Location/Qualifiers
1. .1247
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/mol type="rRNA"
/isolation source="uranium mill tailings, soil sam
/isolation source="uranium mill tailings, soil sam
/isolation source="133"
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/clone_lib="43F-1404R"
/clone_lib="43F-1404R"
/country="USA:Shiprock, New Mexico"
1. .1247
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Bakterielle Diversitaet in Erdproben aus Uranabfallhalden
Unpublished
                                                            1. .936
/organism="uncultured eubacterium WCHAl-16"
/doctype="genomic DNA"
/db xresan:74258"
/clone="WCHAl-16"
/note="isolated from a contaminated aquifer"
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/product="16S ribosomal RNA"
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100.0%; Pred. No. 35;
ive 0; Mismatches
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/product="168 ribosomal RNA"
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Uncultured Chloroflexaceae group bacterium 16S FRNA gene, clone
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Uncultured eubacterium WCHA1-16 16S ribosomal RNA gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-FEB-2001) Nuebel U., Molekulare Systematik und Oekologie, Deuterche Sammlung von Mikroorganismen und Zellkulturen, Mascheroder Weg 1B, Braunschweig, 38124, GERMANY Location/Qualifiers
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AJ309611. GI:15552867
168 ribosomal RNA; 168 rRNA gene.
168 ribosomal RNA; 168 rRNA gene.
uncultured Chloroflexales bacterium
uncultured Chloroflexales bacterium
Bacteria; Chloroflexales; chloroflexales; environmental samples.
1 (bases 1 to 91).
Nubel, C., Bateson, M.M., Madigan, M.T., Kuhl, M. and Ward, D.M.
Diversity and distribution in hypersaline microbial mats of bacteria related to Chloroflexus spp
Appl. Environ. Microbiol. 67 (9), 4365-4371 (2001)
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uncultured eubacterium WCHA1-16
uncultured eubacterium WCHA1-16
l (bases to 36)
Dojka, M.A., Hugenholtz, P., Haack, S. K. and Pace, N. R.
Microbial diversity in a hydrocarbon- and
chlorinated solvent-contaminated aquifer undergoing intribioremediation
Appl. Brivinon. Microbiol. 64 (10), 3869-3877 (1998)
98432811
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/mol_type="genomic DNA"
/mol_type="taxon:152575"
/clone="p4-D01"
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Dojka,M.A. Jr., Hugenholtz,P., Haack,S. and Pace,N.R.
Direct Submission
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100.0%; Score 20; DB 1; Length 911;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels
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      GGAGGAAGGCGAGGATGACG 799
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/gene="16S rRNA"
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AF050608.1 GI:2967784
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Uncultured Eubacteriaceae bacterium gene for 16S rRNA, partial sequence, clone:R8-M13.
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AB088955.1 GI:27530167
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Submitted (3-701. 2002) Yuichi Hongoh, Japan Science and Technology
Corporation (3-701. Bio-Recycle Project, International Cooperative
Research Project; Hirosawa 2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:yhongo@postman.riken.go.jp, Tel:81-48-467-9546,
Fax:81-48-462-4672)
Fax:81-48-462-4672
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Uncultured bacterium TA18 16S ribosomal RNA gene, partial sequence.
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/organism="uncultured Bubacteriaceae bacterium"
/mol_type="genomic DNA"
/isolation_source="PCR-derived sequence from termite gut
homogenate"
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uncultured Eubacteriaceae bacterium
Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae;
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Molecular analysis of bacterial microbiota in the gut of the termite Reticulitermes speratus (Isopeara, Rhinotermitidae)
FEMS Microbiol. Bcol. 44, 231-242 (2003)
2 (bases 1 to 1313)
Hongoh,Y., Ohkuma,M. and Kudo,T.
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                                                 100.0%; Score 20; DB 1; Length 1298; 100.0%; Pred. No. 32;
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|db_xref="taxon:203524"
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1 (bases 1 to 1318)
Whu, J.H., Liu, M.T., Tseng, I.C. and Cheng, S.S. Characterization of microbial consortia in a
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/country="Japan:Saitama, Ogose"
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/product="16S ribosomal RNA"
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                                                    AF524023 1255 bp DNA linear BCT 26-DEC-2002 Uncultured bacterium clone FW128 16S ribosomal RNA gene, partial
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Whilins.T.D., Britschgi,T.B., Krest,R.L. and Giovannoni,S.J.
Genetic comparisons reveal the same unknown bacterial lineages in Atlantic and Pacific Bacterioplankton communities
Limnol. Oceanogr. 40 (1), 147-158 (1995)
Original source text: Alpha proteobacterium sp (clone: SAR102) DNA.
Location/Qualifiers
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Brofft, J.B., Shimkets, L.J. and McArthur, J.V.
Direct Submission
Su
                                                                                                                                                                                                                     uncultured bacterium
Bacteria; environmental samples.

[ bases 1 to 1255)
Brofft, J.B., McArthur, J.V. and Shimkets, L.J.
Recovery of novel bacterial diversity from a forested wetland impacted by reject coal and an environmental machine microbiol. 4 (11), 764-769 (2002)
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/mol type="genomic DNA"
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/clone="SAR102"
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/isolation source="forested wetland"
/db.xref="taxon:77133"
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/product="168 ribosomal RNA"
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Helicobacter bovis 16S ribosomal RNA gene, partial sequence.
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                                                                                                             Submitted (01-FEB-2000) Department of Environmental Engineering, National Cheng Kung University, 1 University Road, Tainan 701, Taiwan, ROC
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G Grotche, D, van Boorn, L.-J., Ducatelle, R., Verschuuren, A.,
Tilnant, K., Hessebrouck, F., Quint, W. and Vandamme, P.
Direct Submission
terephthalate-degrading anaerobic granular sludge system
Microbiology 147 (Pt 2), 373-382 (2001)
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/mol type="nost="Bos taurus"
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                                                                                                                                                              Location/Qualifiers

1. 1318
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/clone="TA18"
                                                               2 (bases 1 to 1318)
Wu,J.H., Liu,W.T., Tseng,I.C. and Cheng,S.S.
Direct Submission
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/product="16S ribosomal RNA"
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1103 GGAGGAAGGCGAGGATGACG 1122

1 GGAGGAAGGCGAGGATGACG 20

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August 4, 2004, 04:03:11; Search time 875.663 Seconds (without alignments) 989.948 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                     OM nucleic - nucleic search, using sw model
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1: gb\_ba:\*

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28: em\_htg\_hum:\*

29: em\_htg\_hum:\*

31: em\_htg\_hum:\*

33: em\_htg\_pvi:\*

33: em\_htg\_pvi:\*

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36: em\_htg\_omus:\*

37: em\_htg\_omus:\*

36: em\_htg\_omus:\*

37: em\_htg\_omus:\*

38: em\_htg\_omus:\*

41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES  Description	9	6 AX709025	47 6 BD140316	29 I MCOL6SR2	31 1 TAMRRD01	31 1 TAMRRDB02	31 I VIBIGERII 33 1 TAMBEDAO	37 1 CLO16SRNAA M98449	37 1 LPNRRDC02 M19444	37 6 E05154 E05154	40 1 LPNBMRRNO2	40 1 LPNDTRRN02 M24642	50 1 VIBLESR12 D11248	55 1 AEOS16SR D11224	64 1 TAMRRN02 M34713	76 1 D28568S2 D28569	76 1 D28571S2 76 1 D28574S2	76 1 VIB16SR10 D11246	78 1 PHRL16SR D11233 82 1 AFOH16SR2 D11219	83 1 UOU46521 U46521	88 1 AY373834 AY37383 89 1 AY373835	91 1 VIBIGRA20 D11256	91 6 AX5/5429 AX5/5429 92 1 AF045813 AF045813	93 1 AF228141 AF228141	93 1 AF228145 AF228145 95 6 128355 S	95 6 BD011645 BD011645	96 I AF045815 AF04581 00 1 AF045823 AF04582	00 1 UBA421167 AJ421167	00 1 UEU405022 03 1 AF045827 AF04582	06 1 ALTH16SR2 07 1 AROM16SP	207 1 LARPLESR2 207 1 VIBLESR13 D11249 Vibrio co	ALIGNMENTS		23 bp DNA linear PAT 07-JAN from Patent WO02077271.	GI:27552061	construct	onstruct sequences.	h.D. and Schramm, C.
Query	Marcin	0.001.0	100		1001	100.	100	1001	100.	1001	1001	100.	1000	100.	100.	100.	1001	100.	001	1001	100.	001	100	100	1001	100	1001	100.	100.	100.	0.001			AX575427 Sequence 2	K575427 K575427.1		synthetic artificial	I Vollenbroich, D. and
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Kita-Tsukamoto, K.
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16S ribosomal RNA.
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PR 31-MAY-1989 US 359158
PI DAVID J LANE, YOTSNA SHAH, AMELIA BUHARIN, WILLIAM G WEISBURG PC C1201/68, C12N15/09, C12N15/09, C12N15/00, CC Synthesized probe for hybridization
                                                                                                                                                                                                                                                                                           PAT 04-APR-2003
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synthetic construct
artificial sequences.

1 (bases 1 to 47)
Lane, D.J., Shah, J., Buharin, A. and Weisburg, W.G.
Universal cubacteria nucleic acid probe and method
Patent: JP 2002051799-A 9 19-FEB-2002;
Shrificial Sequence
PD 19-FEB-2002
                                                                                                                  ch 100.0%; Score 20; DB 6; Length 23; Similarity 100.0%; Pred. No. 1.6e+05; 20; Conservative 0; Mismatches
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47 bp DNA linear Universal eubacteria nucleic acid probe and method. BD140316
BD140316.1 GI:23235261
JP 2002051799-A/9.
                             1. .23
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/noTe="Primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="synthetic construct"
/mol_type="unassigned DNA"
/mol_txref="taxon:32630"
/noce="primer"
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Sequence 1 from Patent WOO3014382.
AX709025
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 Minerva Biolabs GmbH (DE)
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artificial sequences.
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L.pneumophila (strain Chicago-2) 16S rRNA, partial, segment 2 of 3.
M19442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (30-APR-1992) Kumiko Kita-Tsukamoto, University of Tokyo,
Ocean Research Institute; 1-15-1 Minamidai, Nakano-ku, Tokyo 164,
Japan (E-mail:tukamoto@aix3.ori.u-tokyo.ac.jp, Tel:03-3376-1251,
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Kita-Tsukamoto.K., Oyaizu,H., Nanba,K. and Simidu,U.
Phylogenetic relationships of marine bacteria, mainly members of
the family Vibrionaceae, determined on the basis of 16S rRNA
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Legionella pneumophila
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
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/organism='Artificial Sequence'
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93152464
                                                                                                                                                                                                      100.0%; Score 20; DB 6; I
llarity 100.0%; Pred. No. 1.1e+05;
Conservative 0; Mismatches 0;
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    .47
    Organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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/strain="IAM12914"
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Tatlockia micdadei
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Tatlockia.
1 (bases 1 to 131)
Fox, K., Brown, A. and Schnitzer, G.
Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
                                                          AMRRDB02 131 bp rRNA linear BCT 23-JUL-1993 micdadei (strain Pgh-12) 16S rRNA, partial, segment 2 of 3.
                                                                                                                                                                                                                                                                                                                                                                             Brown, A., Fox, K.F. and Schnitzer, G. Tatlockia, a genetically and chemically distinct group of bacteria: Proposal to transfer Legionella maceachernii (Brenner, et al.) to the genus Tatlockia as Tatlockia maceachernii comb. nov Syst. Appl. Microbiol. 14, 52-56 (1991) Octiginal source text: T.micdadei (ATCC 33346; strain Pgh-12) ribosomal RNA.
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Kita-Tsukamoto, K.
Direct Submisteion
Submitted (30-APR-1992) Kumiko Kita-Tsukamoto, University of Tokyo,
Coean Research Institute; 1-15-1 Minamidai, Nakano-ku, Tokyo 164,
Japan (B-mail:tukamotogaix3.ori.u-tokyo.ac.jp, Tel:03-3376-1251,
Fax:03-3375-6716)
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Kitza-Tsukamoto,K., Oyaizu,H., Nanba,K. and Simidu,U.
Phylogenetic relationships of marine bacteria, mainly members the family Vibrionaceae, determined on the basis of 16S rRNA
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Vibrio cholerae
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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2 (sites)
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/organism="Vibrio cholerae"
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/db_xref="taxon:451"
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M19446.1 GI:176105
16S ribosomal RNA.
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                1 (bases 1 to 131)
Fox,K., Brown,A. and Schnitzer,G.
Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
                                                                                                                                Erown, A., Fox, K.F. and Schnitzer, G.
Tatlockia, a genetically and chemically distinct group of bacteria:
Proposal to transfer Legionella maceachernii (Brenner, et al.) to
the genus Tatlockia as Tatlockia maceachernii comb. nov
Syst. Appl. Microbiol. 14, 52-56 (1991)
Original source text: L.pneumophila (ATCC 33215; strain Chicago-2)
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1 (Basea 1 to 131)

Fox.K., Brown,A. and Schnitzer,G.
Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic implications
Syst. Appl. Microbiol. 11, 135-139 (1989)
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Tatlockia, a genetically and chemically distinct group of bacteria:
Proposal to transfer Legionella maceachernii (Brenner, et al.) to
the genus Tatlockia as Tatlockia maceachernii comb. nov
Syst. Appl. Microbiol. 14, 52-56 (1991)
Original source text: T.micdadei (strain PPA-JC) ribosomal RNA.
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Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 20; Conservative 0; Mismatches 0; Indels
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2 (sites)
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/product="16S ribosomal RNA"
About 250 bp after segment 1.
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/product="16S ribosomal RNA"
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T.micdadei (strain,PPA-JC) 168
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/db_xref="taxon:446"
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/db_xref="taxon:451"
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M19451.1 GI:176096
16S ribosomal RNA.
1 of 3
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Appl. Microbiol. Biotechnol. 39 (4-5), 553-557 (1993)
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2 (sites)
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Brown, A., Fox, K.F. and Schnitzer. G.
Brown, A., a genetically and chemically distinct group of bacteria:
Proposal to transfer Legionella maceachernii (Brenner, et al.) to
the genus Tatlockia as Tatlockia maceachernii comb. nov
syst. Appl. Microbiol. 14, 52-56 (1991)
Original source text: T.micdadei (ATCC 33218; strain TATLOCK)
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Clostridium sp. 16S ribosomal RNA (16S rRNA) gene, partial
sequence.
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Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
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M984491 GI:144701
16S ribosomal RNA.
Clostridium sp.
Clostridium sp.
Bacteria; Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
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Galindo, I., Rangel-Aldao, R. and Ramirez, J.L.
A combined polymerase chain reaction-colour development
hybridization assay in a microtitre format for the detection of
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Tatlockia micdadei
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Tatlockia.
1 (bases 1 to 133)
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100.0%; Score 20; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 20; Conservative 0; Mismatches 0; Indels
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ilarity 100.0%; Pred. No. 5.9e+04;
Conservative 0; Mismatches 0;
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/mol_type="rRNA"
/db_xreff="taxon:451"
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   /mol_type="rRNA"
/strain="IID 935"
/db_xref="taxon:666"
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168 ribosomal RNA.
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Brown, A., Fox, K.F. and Schnitzer, G.
Tatlockia, a genetically and chemically distinct group of bacteria:
Proposal to transfer Legionella maceachernii (Brenner, et al.) to
the genus Tatlockia as Tatlockia maceachernii comb. nov
syst. Appl. Microbiol. 14, 52-56 (1991)
Original source text: L.pheumophila pheumophila (ATCC 33152; strain
'Philadelphia-i) ribosomal RNA.
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Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
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L pneumophila (strain Philadelphia-1) 16S rRNA, partial, segment 2
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Bacteria; Froteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Legionella.
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/mol_type="rRNA"
/db_xref="taxon:446"
-dl_>137
/product="16S ribosomal RNA"
About 250 bp after segment 1.
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100.0%; Pred. No. 5.8e+04;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 20; Conservative 0; Mismatches 0;
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2 (sites)
Original source text: Clostridium sp. Maracabo) (library: EMBL4-LBB) DNA. Location/Qualifiers
                                                                                         /mol_type="unassigned DNA"
/db_xref="taxon:1506"
                                                                                                                                                                                                         <1. .>137
/gene="16S rRNA"
/product="16S ribosomal RNA"
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M19444.1 GI:175178
16S ribosomal RNA.
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Best Local Similarity 100.
Matches 20; Conservative
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Fox, K., Brown, A. and Schnitzer, G.
Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
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2 (bases 1 to 140)

Brown, A., Fox, K.F. and Schnitzer, G.

Tatlockia, a genetically and chemically distinct group of bacteria:

Proposal to transfer Legionella maceachernii (Brenner, et al.) to
the genus Tatlockia as Tatlockia maceachernii comb. nov
syst. Appl. Microbiol. 14, 52-56 (1991)

Original source text: Fluoribacter bozemanae (strain MI-15) rRNA.
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Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
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Legionellaceae; Fluoribacter.
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16S ribosomal RNA; ribosomal RNA small subunit.
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165 ribosomal RNA; ribosomal RNA small subunit.
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About 243 bp after segment 1.
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E05154 117 bp DNA linear PAT 29-SEP-1997 Sequence of a DNA fraction prepared by a restriction enzyme HAP II from DNA coding for E.coli 16S ribosome RNA.
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                                              E05154
E05154.1 GI:2173347
UP 19931247-A/26.
UP 19931247-A/26.
Escherichia coli
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Escherichia coli
Encerobacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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16S ribosomal DNA.
Clostridium butyricum
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Clostridium cutes; Clostridia; Clostridiales; Clostridiaceae;
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Galindo,I., Rangel-Aldao,R. and Ramirez,J.L.
Galindo,I., Rangel-Aldao,R. and Ramirez,J.L.
A combined polymerase chain reaction-colour development
hybridization assay in a microtitre format for the detection of
Clostridium spp
Appl. Microbiol. Biotechnol. 39 (4-5), 553-557 (1993)
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Galindo-Castro, I.F., Rangel, R. and Ramirez, J.L.
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Clostridium butyricum 16S ribosomal DNA gene.
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/mol_type="unassigned DNA"
/db_xref="taxon:1492"
                                                                                                                                                                                                                 METHOD FOR SPECIFYING DNA BASE SEQUENCE
Patent: JP 1993192147-A 26 03-AUG-1993;
KIRIN BIBARETSUJI KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
                                                                                                                                                                                                                                                                     Escherichia coli
JP 199192147-A/26
03-AUG-1993
15-NOV-1991 JP 1991300882
15-NOV-1991 JP 1991300882
SHIRASU YOSHIHARU
CLENIS/00, CLEQL/66, CLEDL/68;
strandedness: Double;
topology: Linear;
topology: Linear;
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AUTHORS Brown, A., Fox, K.F. and Schnitzer, G.

TITLE Tatlockia, a genetically and chemically distinct group of bacteria:
Proposal to transfer Legionella maceachernii (Brenner, et al.) to
the genus Tatlockia as Tatlockia maceachernii comb. nov

JOURNAL Syst. Appl. Microbiol. 14, 52-56 (1991)

COMMENT Appl. Microbiol. 14, 52-56 (1991)

COMMENT Comail RNA.

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Post-processing: Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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6747726

Database :

N\_Geneseq\_29Jan04:\*
1: geneseqn1980s:\*
2: geneseqn1990s:\*
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## STIMMARTES

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Result No.	Score	Query Match	Length	DB	ID	Description	e o	
				:				
Н	20	100.0	23	7	ABV74328		Mycoplasm	
7	20	100.0	24	٣	AAA39031	Aaa39031 1	Unknown b	
ო	20	100.0	37	ω	ABX94830	Abx94830	16S rRNA	
4	20	100.0	37	ω	ABX94859	Abx94859	16S rRNA	
O S	20	100.0	47	7	AAQ10118		Probe 173	
9	20	100.0	50	9	ABL59813	m	Enterococ	
7	20	100.0	20	9	ABL59817		Peptostre	
00	20	100.0	50	9	ABL59820		Chlamydia	
σι	20	100.0	50	9	ABL59819		Fusobacte	
10	20	100.0	50	9	ABL59786	Ab159786	Campyloba	
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17	20	100.0	20	9	ABL59795		Escherich	
18	20	100.0	50	v	ABL59812		Listeria	
19	50	100.0	20	ø	ABL59816	Ab159816 (	Clostridi	
20	20	100.0	20	9	ABL59804	_	Wolbachia	
21	20	100.0	50	9	ABL59790		Leptothri	
22	20	100.0	20	Q	ABL59788		Treponema	
23	20	100.0	20	ø	ABL59803	Ab159803 1	Nitrobact	

## ALIGNMENTS

RESULT 1

Mollicutes sp; Mycoplasma; 16S rRNA; infection; PCR; primer; ss. Mycoplasma 16S rRNA gene PCR primer SEQ ID NO 2. BP. 25-MAR-2002; 2002WO-DE001154. 25-MAR-2001; 2001DE-01015749. (MINE-) MINERVA BIOLABS GMBH. Schramm C; ABV74328 standard; DNA; 23 29-JAN-2003 (first entry) WPI; 2003-040591/03. Vollenbroich D, WO200277271-A2. Mycoplasma sp. 03-OCT-2002. ABV74328; ABV74328 

Control plasmid, useful as internal standard in amplification method for detecting Mycoplasma, contains primers that recognize parts of the Mycoplasma 16S rRNA gene.

Claim 2; Page 15; 25pp; German.

The invention relates to a control plasmid (A) containing: (a) primers that recognize a segment of the 16S rRNA-encoding gene in the Mycoplasma segmence (i) and (b) between the primers an amplicon that includes the sequence (i). (A) is used as a control in a PCR method for detections of Mycoplasma in biological materials, e.g. for diagnosing infections or control for PCR detection of cell cultures. (A) provides an internal control for PCR detection of Mycoplasma to exclude false negatives. The method is more sensitive and specific than known processes, providing reliable detection of even very low titers of Mycoplasma and when used in real-time PCR, has a broad dynamic and linear measurement range, allowing accurate quantitation. The present sequence is that of a Mycoplasma 16S rNNA gene PCR primer of the invention

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Gaps

Sequence 24 BP; 9 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

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The present invention describes a method for identifying a microorganism by comparing a composite sequence (I) of a ribosomal RNA gene region with a sequence of unknown microorganisms in a database and identifying the region in the database that matches with (I). (I) is generated by simultaneously obtaining nucleotide base sequence data from every copy of the rRNA gene region in the genome of the unknown microorganism. Also described is a method for identifying the species of microorganism by generating (I) and entering it into a first data register of a programmable computer, comparing the first data register with reference data registers that encode a unique composite rRNA sequence corresponding to (I) and correlated with unique microorganism species name, and displaying the unique microorganism name ocorrelated with the best matching first data register. The method is useful for identifying microorganisms which are useful in a variety of fields including human medicine, veterinary medicine, agriculture, food science and industrial microbiology. The microorganisms found in patients suffering from an infectious disease can also be identified.
                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial; 16S rRNA; identification; polymorphism; microorganism; classification; primer; human medicine; veterinary medicine; agriculture; food science; industrial microbiology; infectious disease; food safety;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying an unknown microorganism by generating a composite sequence of its ribosomal RNA gene region and comparing with composite ribosomal RNA region sequences of distinct microorganisms in a database.
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0
                                                 DB 7; Length 23;
                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                         Unknown bacterial 16S rRNA gene primer 0776F SEQ ID NO:9.
               Sequence 23 BP; 9 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
                                           ilarity 100.0%; Score 20; DB 7 ilarity 100.0%; Pred. No. 0.1; Conservative 0; Mismatches
                                                                                                                             1 GCAAACAGGATTAGATACCC 20
                                                                                                                                                       GCAAACAGGATTAGATACCC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example, Col 10; 11pp; English.
                                                                                                                                                                                                                                                             AAA39031 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00073465.
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                                                                                                                                                                                                                                                                                                                                       25-AUG-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith DH, Dodge DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-338488/29.
                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                   Query Match
Best Local Simi
Matches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1997;
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AAA39031
ID AAA3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aspects of analytical quality can be included. This sequence represents an oligonuclectide associated with the detection of 165 rRNA from various bacterial samples, which is used to illustrate the device of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Device for determining analytes, useful e.g. for detecting bacteria that cause parodontitis, comprises a surface with immobilized analytical and
                                                                                                                                                                                                                                                                                                                                                           Probe, detection, primer; 16S rRNA, amplification; parodontitis; SNP; gene expression pattern; single-nucleotide polymorphism; ss.
                                      Gaps
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100.0%; Score 20; DB 3; Length 24; 100.0%; Pred. No. 0.1; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 20; DB B; Length 37; 100.0%; Pred. No. 0.099; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ronacher B, Winner F, Zehethofer K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37 BP; 11 A; 8 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LAMB-) LAMBDA LABOR MOLEKULARBIOLOGISCHE.
                                                                                                                                                                                                                                                                                                                           16S rRNA forward PCR primer SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 26; 51pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacterial samples, which is used
                                                                            1 GCAAACAGGATTAGATACCC 20
                                                                                                          2 GCAAACAGGATTAGATACCC 21
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                                    0;
                                                                                                                                                                                                              ABX94830 standard; DNA; 37 BP
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                                                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity 100.
Matches 20; Conservative
                                          Conservative
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                  Local Similarity
es 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       Inidentified.
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    Query Match
                                          Matches
                                                                                                                                                                        RESULT 3
ABX94830
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testing for pathogens. Plants harbouring phytopathogenic bacteria are also identified. The method is convenient and efficient as there is no need to isolate one or more individual 16S rRNA genes. AAA39023 to AAA3039 represent primers for the 16S rRNA gene, which are used in the exemplification of the present invention

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Nucleic acid probes - specific for RNA of Eubacteria, for use in clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probes allow assay for Bubacteria to be carried out in clinical samples such as blood or urine, in a cost effective and fast manner. The probes require only small sample sizes which may be amplified, with some of the probes suitable as primers. (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection, microorganism, 16S rDNA, 16S rRNA, identification, gene, microbial encephalitis, viral encephalitis, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      f match 100.0%; Score 20; DB 2; Length 47; Local Similarity 100.0%; Pred. No. 0.098; les 20; Conservative n. Minner.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis 16S rDNA fragment #3
                                                                                                 Probe 1739 to the 16s rRNA of Eubacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 14-16; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Weisburg WG;
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                   (revised)
(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              (GENE-) GENE-TRAK SYST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-007226/01.
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                                                                                                                                             ribosomal RNA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200210444-A1
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                   27-AUG-2003
09-JAN-2003
14-MAR-1991
                                                                                                                                                                                                                            WO9015157-A
                                                                                                                                                                                                                                                                      13-DEC-1990,
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                                                                                                                                                                                     Eubacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Lane DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel device for detecting analytes in a sample. The device comprises a carrier surface which contains at least one analytical region (including at least one immobilised binding partner for the analyte) and at least one control region which controls of the quality of analysis. The device is particularly used for nucleic acid amplification and detection of (i) bacterial species associated with parodontitis, (ii) gene expression patterns and (iii) single-nucleotide polymorphisms (SNP's). The device provides reproducible, rapid and simple analysis of rucleic acid sequences. The control system is subjected to exactly the same series of operations as the analytical regions, so no extra time for the control step is required and system costs are not significantly more than for analysis without a control. If the device is stored for archiving, the control results are also saved. Many different analytes can be detected simultaneously and controls for many different analytes an oligomucleotide associated with the detection of 165 rRNA from various bacterial samples, which is used to illustrate the device of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Device for determining analytes, useful e.g. for detecting bacteria that cause parodontitis, comprises a surface with immobilized analytical and control agents.
                                                                                                                                                                                                                                                                      Probe; detection; primer; 16S rRNA; amplification; parodontitis; SNP; gene expression pattern; single-nucleotide polymorphism; ss.
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                                                                                                                                                                                                                          16S rRNA detection associated positive control oligonucleotide #3.
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100.0%; Score 20; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LAMB-) LAMBDA LABOR MOLEKULARBIOLOGISCHE.
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GCAAACAGGATTAGATACCC 25
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                                                                                                   ABX94859 standard; DNA; 37 BP.
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                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                       11-JUL-2003
                                                                                                                                                                                                                                                                                                                                    Unidentified
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AAQ10118;

RESULT 5 AAQ10118/C ID AAQ1011 XX AC AAQ1011

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20-FEB-2003

ABX94859;

ABX94859 RESULT

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Detection, microorganism, 16S rDNA, 16S rRNA, identification, gene, microbial encephalitis, viral encephalitis, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                        Peptostreptococcus micros 16S rDNA fragment #3.
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                  exemplification of the present invention
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                                                         Example 12; Fig 1C; 101pp; English.
                                                                                                                                                                                                                                                                                                                      GCAACAGGATTAGATACCC 35
                                                                                                                                                                                                                                                                                                           1 GCAAACAGGATTAGATACCC 20
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Best Local Similarity
Local Similarity
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       WPI; 2002-404428/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -WO200210444-A1.
                                           microorganism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hunter N,
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The present invention describes a mechanical content in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microbial content in a sample, conserved amongst 2 or more species of microorganisms. Also describes is an isolated polynucleotide (I) or its complement having a nuclectide sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of microorganism. (I) can be used: (I) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus in a sample; and (3) as a probe control microbial derived target material; in assessing encephalitis and identify microorganisms at the genus or species level, and as a trap for identify microorganisms at the genus or species level, and as a trap for identify microorganism and viral encephalitis. (I) is applicable to a range of industries including the medical, adricultural and user and the microbial and viral encephalitis. (I) is and industrial industries with specific uses including enviroprotection, bloremediation, medical diagnosis, water quality control or food quality control. (I) provides an ability to detect bacteria from samples which undetected or under-estimated by viable culture count methods and enables rapid differentiation of bacteria from viral infections within the clinical situations. ABLS902 to ABLS9821 represent les rDNA fragments, and in the
                                                                                                                                 Polymucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention describes a method for determining the total
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                                                                                                                                                                                                                                                                                                                                                                            Example 12; Fig 1C; 101pp; English.
                                       WPI; 2002-404428/43.
                                                                                                                                                                                                                                                                                            microorganism.
The present invention describes a method for determining the total microbial content in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microorganisms. Also describes is an isolated polynucleotide (I) or its complement having a nucleotide sequence which is comprised by 16S rDNA or 16S rENA, substantially conserved amongst two or more species of microorganism. It is an a sample, (2) as a primer or probe for identifying a microorganism by its genus in a sample, and (3) as a probe for identifying a particular microorganism or prevalence of a particular genus or species of microorganism by its genus in a sample, and (3) as a probe for identifying a particular microorganism or prevalence of a particular genus or species of microorganism or prevalence of a particular genus or species of microorganism, in a sample, (1) can also be used to identify microbial and viral encephalitis. (1) is applicable to a range of industries including the medical, agricultural applicable to a range of industries including the medical, agricultural biconemication, medical diagnosis, water quality control or food quality control. (1) provides an ability to detect bacteria from samples which repetited or under-estimated by viable culture count methods and enables rapid differentiation of bacteria from viral infections within the rapid of the particular of the partic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    limited time constraints sometimes experienced in life-threatening
Linical situations. ABLS9702 to ABLS9821 represent 16S rDNA fragments,
and ABLS9822 to ABLS9830 represent primers and probes, used in the
                                                                                                                                      Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 50 BP; 14 A; 12 C; 16 G; 8 T; 0 U; 0 Other;
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Chlamydia trachomatis 16S rDNA fragment #3. 16 GCAAACAGGATTAGATACCC 35 1 GCAAACAGGATTAGATACCC 20 ABL59820 standard; DNA; 50 BP (first entry) Query Match Best Local Similarity 100. Matches 20; Conservative Chlamydia trachomatis 18-JUL-2002 ABL5982( à q Gaps . 100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098; 0; Indels

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                  Gaps
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100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                               27-JUL-2001; 2001WO-AU000933.
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Nadkarni MA;

Martin FE,

Jacques NA,

Hunter N,

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The present invention describes a method for determining the total microbial content in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microorganisms. Also describes is an isolated polynucleotide (1) or its complement having a nucleotide sequence which is comprised by 168 rDNA or 168 rRNA, substantially conserved amongst two or more species of microorganism. (1) can be used: (1) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus or prevalence of a particular correct an microbial-derived target material; in asample; and sa a trap for identify microbial-derived target material; in can assessing encephalitis and distinguishing between microbial and viral encephalitis. (1) is applicable to a range of industries including the medical, agricultural advisition didistries with specific uses including enviroprotection, bioremediation, medical diagnosis, water quality control or food quality control. (1) provides an ability to detect bacteria from samples which industrial to cultivate and that would in all practically remain undetected or under-estimated by viable culture count methods and enables rapid differentiation of bacteria from viral infections within the limited ime constraints sometimes experienced in life-threatening clinical situations. ABIS9702 to ABIS9821 represent 16s rDNA fragments, exemplification of the present invention
                                                            Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection, microorganism; 16S rDNA; 16S rRNA; identification, gene, microbial encephalitis; viral encephalitis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 50 BP; 15 A; 11 C; 16 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusobacterium nucleatum 168 rDNA fragment #3.
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                                                                                                                                                                         Example 12; Fig 1C; 101pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL59819 standard; DNA; 50 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusobacterium nucleatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hunter N, Jacques NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UNSY ) UNIV SYDNEY.
                    WPI; 2002-404428/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 20; Conserv
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                                                                                                                                  microorganism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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The present line describes a meriou for determining the recent microbial content in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microbian anucleotide sequence which is comprised by 16s rbNa compresent having a nucleotide sequence which is comprised by 16s rbNa or 16s rRNa, substantially conserved amongst two or more species of microbial content in a sample; 13 as a primer or probe for determining the total microbial content in a sample; 13 as a primer or probe for dentifying a microbial micropianism or prevalence of a particular of for identifying a particular microorganism; in a sample; (1) can also be used to identify microorganisms at the genus or species level, and as a trap for total microbial derived target material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (1) is applicable to a range of industries including the medical, agricultural and industries with specific uses including enviroprotection, bioremediation, medical diagnosis, water quality control or food quality control. (1) provides an ability to detect bacteria from samples which are difficult to cultivate and that would in all practicality remain cunderected or under-estimated by viable culture count methods and enables rapid differentiation of bacteria from viral infections within the limited time constraints sometimes experienced in life-threatening clinited time constraints experienced in life-threatening clinited limited is represent primers and probes, used in the
                                                         Polynuclectide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rNNA, substantially conserved amongst two or more species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                           present invention describes a method for determining the total
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098; o; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 50 BP; 14 A; 12 C; 16 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campylobacter jejuni 168 rDNA fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention
                                                                                                                                                                    Example 12; Fig 1C; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCAAACAGGATTAGATACCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100.0%; P 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL59786 standard; DNA; 50 BP.
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Best Local Similarity
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                                                                                                                               microorganism
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ABL59786
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microbial content in assmile, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microorganisms. Also describes is an isolated polynucleotide (1) or its complement having a nucleotide sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of microorganism. (1) can be used: (1) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus in a sample; and (3) as a probe for identifying a particular microorganism or prevalence of a particular genus or species level, and as a trap for identify microbial-derived target material; in assessing encephalitis and identify microbial-derived target material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (1) is applicable to a range of industries including the medical, agricultural and industrial industries with specific uses including enviroprotection, bloremediation, medical diagnosis, water quality control or food quality control. (1) provides an ability to detect bacteria from samples which undetected or under-estimated by viable culture count methods and enables capital affections. ABLS9821 represent lefs round in the infections within the limited time constraints sometimes experienced in life-threatening control of the present primers and probes, used in the constraint of the property of the primers and probes, used in the
                                                          Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection, microorganism; 16S rDNA; 16S rRNA; identification; gene; microbial encephalitis; viral encephalitis; ds.
                                                                                                                                                                                                             The present invention describes a method for determining the total
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 50 BP; 14 A; 13 C; 16 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exemplification of the present invention
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                                                                                                                                                                Example 12; Fig 1C; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCAAACAGGATTAGATACCC 20
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                    WPI; 2002-404428/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                          microorganism.
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microbial content in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microorganisms. Also describes is an isolated polynucleotide (1) or its complement having a nucleotide sequence which is comprised by 165 rDNA or 165 rRNA, substantially conserved amongst two or more species of microorganism. (1) can be used: (1) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for dentifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism, in a sample; (1) can also be used to identifying a particular microorganism, in a sample; (1) can also be used to identify microorganisms at the genus or species level, and as a trap for total microbial-derived target material; in assessing encephalitis and distributing between microbial and viral encephalitis. (1) is carriagisable to a range of industries including the medical, agricultural and industrial industries with specific uses including enviroprotection, bioremediation, medical daganosis, water quality control or food quality control. (1) provides an ability to detect bacteria from samples which are difficult to cultivate and that would in all practicality remain and affice and an enables of the province of the control or control or food quality or and afficult to cultivate and that would in all practicality in the nables of the control or food and enables or the control or food province of the control or foo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rapid differentiation of bacteria from viral infections within the limited time constraints sometimes experienced in life-threatening clinical situations. ABLS902 to ABLS9021 represent 165 rDNA fragments, and ABLS9022 to ABLS9030 represent primers and probes, used in the
                                                                     Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                             present invention describes a method for determining the total
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50 BP; 14 A; 13 C; 16 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori 16S rDNA fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the present invention
                                                                                                                                                                                                     Example 12; Fig 1C; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCAAACAGGATTAGATACCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                      WPI; 2002-404428/43
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                                                                                                                                                      microorganism.
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Best Local &
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Gaps

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Martin FE, Nadkarni MA;

Jacques NA,

Hunter N,

(UNSY ) UNIV SYDNEY

27-JUL-2001; 2001WO-AU000933. 28-JUL-2000; 2000AU-00009090.

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Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 168 rDNA or 168 rRNA, substantially conserved amongst two or more species of

WPI; 2002-404428/43.

The present invention describes a method for determining the total

Example 12; Fig 1C; 101pp; English.

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Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene; microbial encephalitis; viral encephalitis; ds.
                                                                                                                                                                                                                                                               100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098;
                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     Salmonella typhi 16S rDNA fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martin FE,
                                                                                                                                                                                                                                                                                            1 GCAAACAGGATTAGATACCC 20
                                                                                                                                                                                                                                                                                                        16 GCAAACAGGATTAGATACCC 35
                                                                                                                                                                                                                                                                                                                                            ABL59796 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUL-2001; 2001WO-AU000933
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                                                                                                                                                                                                                                                                                                                                                                        18-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                        Local Similarity 100.
les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hunter N, Jacques NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNSY ) UNIV SYDNEY.
      WPI; 2002-404428/43.
                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200210444-A1.
                                        microorganism.
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                                                                                                                                                                                                                                                                                                                                                           ABL59796;
                                                                                                                                                                                                                                                                  Query Match
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Matches
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Gaps

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microbial content in a sample, comparising amplifying a target nucleotide microbial content in a sample, comparising amplifying a target nucleotide comparisons. Also describes is an isolated polynucleotide (I) or its complement having a nucleotide sequence which is comprised by 165 rDNA or 165 rENA, substantially conserved amongst two or more species of microorganism. (I) can be used: (1) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for determining the total microbial content in a sample; and (3) as a probe for determining the total microbial content in a sample; and (3) as a probe for determining a microbial content in a sample; and (3) as a probe for determining the total microbial and incorporation. (I) can also be used to identify microorganisms at the genus or species level, and as a trap for otal microbial-derived target material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (I) is applicable to a range of industries including the medical, agricultural applicable to a range of industries including the medical, agricultural control, medical diagnosis, water quality control or food quality control. (I) provides an ability to detect bacteria from samples which care difficult to cultivate and that would in all practicality remain cundetected or under-estimated by viable culture count methods and climited time constraints sometimes experienced in life-threatening climited the constraints sometimes experienced in life-threatening climited the constraints sometimes experienced in life-threatening climited situations. ABLS99021 to ABLS9921 represent 165 rDNA fragments, very complification of the present invention
The present invention describes a method for determining the total

microbial content in a sample, comprising amplifying a target nucleotide

sequence which is substantially conserved amongst. 2 or more species of

microorganisms. Also describes is an isolated polynucleotide (I) or its

complement having a nucleotide sequence which is comprised by 16S rDNA or

CS STRNA, substantially conserved amongst two or more species of

microorganism. (I) can be used: (I) as a primer or probe for determining

the total microbial content in a sample; (2) as a primer or probe for

continuitying a microorganism by its genue in a sample. (I) as a primer or probe for

dentifying a microorganism, in a sample. (I) can also be used to

content species of microorganism, in a sample. (I) can also be used to

content microbial-derived target material; in assessing encephalitis and

content microbial-derived target material; in assessing encephalitis and

distinguishing between microbial and viral encephalitis. (I) is

control. (I) provides an ability to detect bacteria from samples which

are difficult to cultivate and that would in all practicality remain

undetected or under-estimated by viable culture count methods and enables

replied differentiation of bacteria from viral infections within the

rapid differentiation of bacteria from viral infections within the

limited time constraints.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              limited time constraints sometimes experienced in life-threatening clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments, and ABL59822 to ABL59830 represent primers and probes, used in the exemplification of the present invention
                                                                                                                      Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 50 BP; 14 A; 13 C; 16 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                          Example 12; Fig 1C; 101pp; English.
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0
                       100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098;
                                              0; Indels
Sequence 50 BP; 14 A; 12 C; 17 G; 7 T; 0 U; 0 Other;
                                   100.0%; Pred. No. 0.098; ive 0; Mismatches
                                                                                                                                                                                                                        Legionella pneumophila 16S rDNA fragment #3.
                                                                      1 GCAAACAGGATTAGATACCC 20
                                                                                            16 gcaacaggarragaraccc 35
                                                                                                                                                     ABL59799 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                                                                     27-JUL-2001; 2001WO-AU000933.
                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000; 2000AU-00009090.
               Query Match
Best Local Similarity 100...
hes 20; Conservative
                                                                                                                                                                                                    18-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                   Legionella pneumophila
                                                                                                                                                                                                                                                                                                         WO200210444-A1.
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                                                                                                                                                                             ABL59799;
                                                                                                                                 RESULT 14
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Nadkarni MA;

Martin FE,

Jacques NA,

Hunter N,

Nadkarni MA;

(UNSY ) UNIV SYDNEY

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Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rRNA, substantially conserved amongst two or more species of WPI; 2002-404428/43 

Example 12; Fig 1C; 101pp; English.

complement in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microbial content in a sample, conserved amongst 2 or more species of complement having a nucleotide sequence which is comprised by 165 rDNA or 165 complement having a nucleotide sequence which is comprised by 165 rDNA or 165 rRNA, substantially conserved amongst two or more species of microorganism. (1) can be used: (1) as a primer or probe for determining the total microbial content in a sample; (2) as a primer or probe for dentifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism by its genus in sample; and (3) as a probe for identifying a microorganism by its genus or prevalence of a particular genus or species level, and as a trap for identify microorganisms at the genus or species level, and as a trap for identify microorganisms at the genus or species level, and as a trap for identify microbial-derived target material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (1) is a applicable to a range of industries including enviroprotection, bloremediation, medical diagnosis, water quality control or food quality control. (1) provides an ability to detect bacteria from samples which undetected or under-estimated by viable culture count methods and enables capital situations. ABL59702 to ABL59821 represent lefs rbnA fragments, and abL59822 trapresent lefs rbnA fragments, and infinite constraints sometimes experienced in life-threadening capital contents. present invention describes a method for determining the total exemplification of the present invention

Sequence 50 BP; 15 A; 11 C; 16 G; 8 T; 0 U; 0 Other;

100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098; o; Indels ive 0; Mismatches 0; Indels 1 GCAAACAGGATTAGATACCC 20 GCAAACAGGATTAGATACCC 35 20; Conservative Query Match Best Local Similarity Matches g Š

ABL59801 standard; DNA; 50 BP. RESULT 15 ABL59801 HANDER STANDER STANDER

(first entry) 18-JUL-2002 ABL59801;

Caulobacter vibrioides 16S rDNA fragment #3.

Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene; microbial encephalitis; viral encephalitis; ds.

Caulobacter vibrioides

WO200210444-A1

07-FEB-2002.

27-JUL-2001; 2001WO-AU000933.

28-JUL-2000; 2000AU-00009090.

(UNSY ) UNIV SYDNEY

Martin FE, Nadkarni MA; Hunter N, Jacques NA,

Polynucleotide useful as primer or probe for determining microbial content in sample, has sequence which is comprised by 16S rDNA or 16S rNA, substantially conserved amongst two or more species of nicroorganism.

Example 12; Fig 1C; 101pp; English.

microbial content in a sample, comprising amplifying a target nucleotide sequence which is substantially conserved amongst 2 or more species of microbial content in a sample, comprising amplifying a target nucleotide sequence which is comprised (1) or its complement having a nucleotide sequence which is comprised by 16s rDNA or 16s rBNA, substantially conserved amongst two or more species of microorganism. (1) can be used: (1) as a primer or probe for of elemtifying a microorganism by its genus in a sample; and (3) as a primer or probe for cidentifying a microorganism by its genus in a sample; and (3) as a probe for identifying a microorganism in a sample; and (3) as a probe for identifying a microorganism or pevalence of a particular correct in a sample; and (3) as a primer or probe for total microbial derived target material; in assessing encephalitis and distinguishing between microbial and viral encephalitis. (1) is a splicable to a range of industries including the medical, agricultural continual industrial industries with specific uses including enviroprotection, bloremediation, medical diagnosis, water quality control or food quality control. (1) provides an ability to detect bacteria from samples which included difficult to cultivate and that would in all practicality remain undetected or under-estimated by viable culture count methods and enables of industrial from samples which in the control of paretrial from viral infections within the control of paretrial from samples. time constraints sometimes experienced in life-threatening l situations. ABL59702 to ABL59821 represent 16S rDNA fragments, 9822 to ABL59830 represent primers and probes, used in the invention describes a method for determining the total exemplification of the present invention The present clinical imited 

Sequence 50 BP; 14 A; 12 C; 16 G; 8 T; 0 U; 0 Other;

Gaps . 0 100.0%; Score 20; DB 6; Length 50; 100.0%; Pred. No. 0.098; tive 0; Mismatches 0; Indels Conservative Similarity 20; Query Match Local Matches

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